

| Table 121B. Protein Sequence Properties NOV121a | |
|--|--|
| PSort analysis: | 0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen) |
| SignalP analysis: | No Known Signal Sequence Predicted |

A search of the NOV121a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 121C.

| Table 121C. Geneseq Results for NOV121a | | | | |
|--|---|---|--|---------------------|
| Geneseq Identifier | Protein/Organism/Length [Patent #, Date] | NOV121a Residues/ Match Residues | Identities/ Similarities for the Matched Region | Expect Value |
| AAM78688 | Human protein SEQ ID NO 1350 - Homo sapiens, 590 aa. [WO200157190-A2, 09-AUG-2001] | 1..572 10..580 | 388/576 (67%) 449/576 (77%) | 0.0 |
| AAM39343 | Human polypeptide SEQ ID NO 2488 - Homo sapiens, 589 aa. [WO200153312-A1, 26-JUL-2001] | 20..571 37..587 | 331/555 (59%) 404/555 (72%) | 0.0 |
| AAM41129 | Human polypeptide SEQ ID NO 6060 - Homo sapiens, 646 aa. [WO200153312-A1, 26-JUL-2001] | 20..571 94..644 | 331/555 (59%) 404/555 (72%) | 0.0 |
| AAY39920 | Human steroid sulphatase protein sequence - Homo sapiens, 583 aa. [WO9950453-A1, 07-OCT-1999] | 20..569 26..575 | 295/559 (52%) 374/559 (66%) | e-166 |
| AAB51185 | Human sulfatase protein C SEQ ID NO:14 - Homo sapiens, 583 aa. [US6153188-A, 28-NOV-2000] | 20..569 26..575 | 294/559 (52%) 372/559 (65%) | e-165 |

In a BLAST search of public sequence databases, the NOV121a protein was found to have homology to the proteins shown in the BLASTP data in Table 121D.

| Table 121D. Public BLASTP Results for NOV121a | | | | |
|--|--|---|---|---------------------|
| Protein Accession Number | Protein/Organism/Length | NOV121a Residues/ Match Residues | Identities/ Similarities for the Matched Portion | Expect Value |
| P54793 | Arylsulfatase F precursor (EC 3.1.6.-) (ASF) - Homo sapiens (Human), 591 aa. | 1..572 10..581 | 379/577 (65%) 441/577 (75%) | 0.0 |
| AAH20229 | HYPOTHETICAL 64.9 KDA PROTEIN - Homo sapiens (Human), 593 aa. | 4..574 24..593 | 358/574 (62%) 440/574 (76%) | 0.0 |
| P51689 | Arylsulfatase D precursor (EC 3.1.6.-) (ASD) - Homo sapiens (Human), 593 aa. | 4..574 24..593 | 349/574 (60%) 429/574 (73%) | 0.0 |
| P51690 | Arylsulfatase E precursor (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa. | 20..571 37..587 | 334/555 (60%) 405/555 (72%) | 0.0 |
| P08842 | Steryl-sulfatase precursor (EC 3.1.6.2) (Steroid sulfatase) (Steryl- sulfate sulfohydrolase) (Arylsulfatase C) (ASC) - Homo sapiens (Human), 583 aa. | 20..569 26..575 | 295/559 (52%) 374/559 (66%) | e-166 |

PFam analysis predicts that the NOV121a protein contains the domains shown in the Table 121E.

| Table 121E. Domain Analysis of NOV121a | | | |
|---|-----------------------------|--|---------------------|
| Pfam Domain | NOV121a Match Region | Identities/ Similarities for the Matched Region | Expect Value |
| Sulfatase: domain 1 of 1 | 21..504 | 231/530 (44%) 410/530 (77%) | 1e-187 |

Example 122.

The NOV122 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 122A.

Table 122A. NOV122 Sequence Analysis

| | SEQ ID NO: 339 | 3005 bp | |
|---|--|-----------------------|------------------|
| NOV122a, CG59746-01 DNA Sequence | ATTTCTTGGTGTGTCACAGCTGAACCTGCAAAACAGATTGGAACCTCAAGATT ATCAATAATCGGAGATACTGATATTTATTTATTTGAAAGAAAACATGGCTGCCATTCTCC TACGTGGTTTGTCCAATAGGGAACCTGCAAGACTGGGATATCTAAGTCAAAAGAAC ATTCAATTGAGCAGTGGAAAGAAAAGAACAGAAAGTAGACTCGTGTGATTTCAAAAGT GGAAAATATACTACCTTTCGGCTAAGTGATAATTCAAAATGAGTCCTAAATCT ATAGAGGAAACCAAATCACCTGCATTTAACTTACAAAATAATAATGGCTTGT TGAAGGATTATCTCCACAGATGCTGAACAATTGAAAGATATTCTTGACAGAGTTCAT CAAACAGAGGTTCAAGGCACCTGTGAGACCTGTAAGGGGGAGTGTCTTCTAGCA CAACAGAGGAAATCAACAAAACCTTCACTTCCACAAAGTTGATGAGAAAATCAAGTAG CAAATCTTGTGAGATGCAAAAGGAAGTGGGACAGGTGTCTTCAGAGGATGCC CTTACATCAAATTGACACTTACTTGGAGACTTACAGAAAATCAGCACAGAAGA GGAAAAGAATGCTCATCTAGCTCAGAGATGAATGAGGAATTCTTAAAGAAAATAA TTCTGAGAAATCAAGAAATCCAAGGCAGATTGTTGAGGTTGTGAAAGCTATAATCGA GAGAAACAAATTGAGTAAAAGAGTTAGAAGAGATAAGAAATTGGAATGTGAATCTT CATGCATCATGAAACGCCACTGGAAATCTTCACTTACAGATGACATTGGCTCTCAAGC TCTCACTGAGAAAATGTTTGTGATTCTGTTACAACAGGTATACTGACGGTTAC ACAAAGTGGATAAATTAAAACCTTATTTTGAAATTATTCAGAGAAAATATGCCACG GCCCTCCCACATTGGAAACACCCTGTTATGATGCACTGTTACAGTCTACTTT AATCCCATGTTGCTGATGTTACTTAACTCAGATGTTCCATGGGTAATTCCC CTTAATGCTTACCATGCTGTTGACGGCTACTTTTAAAGATACTATAATA TAGAAATCAAGGAGATGTTACTCTGAATCTAAAAGGCATTTCAGCAGCTGCAGA GATATTCCATGGCAATGCACAGAACGATGCTCATGAGTTTAGCTACTGTTAGAT CAACTGAAAGATAACATGGAAAACCTCAACACAATTGGAAGCCTAAAGTGAATTG GGGAAGATAATTCTAACAGGTTTGTGATGACCTGACACCGAGGGTTTC TTGGCCCTGTCATTACTAATTGGTGTAGGTTGACTCCATTGCTTGTAAAGCT TGTGTCAGGTTATCTCAAGACAGACTGAATATTACCTCTCATCAACCTCCCC AAAAGATAAAAGCACATCTTCATCTATTCACTACTTTGATCTTTGGAGC AGAAGAGCTGAGTAAATGTGCAAATGTGAGCACAAGACTTCGTTGGAGTGCAC TCATTCAGTAGGCTACCTAGAATCTTATTGTTACCTCAAACGCTATACTGTTGAATG ACTTTGTCATTAAAGAGAATGACCGAGAATCATTCAACATTAAAGGT GTCTCTCATGCAATGAGGCCACAGCACCTCTCCCTGAGTGAGGATGGGAGAA ATTACAGATTTCACATTAAAAGTTATCGAAAGATGACTTCTGAAACATCAGTG TATCATGGCCTGCAACAAAGGAATCCAAGAGATATCTGGCTCACATTGGATCAGA TAAGGAGTCTGACAAAAAAAGGCCAGACAGTCTTAAAGGGCAAGCAGAACAG CAGCAAAGTACCTGGAAAAAAATTCTAAACCAAAATGAGCTAGAATCTGTACTCAG GAGATCAGGATTCTGGAAAAAGAAGCTGTCACCTAATGAGCTATCTGGAGA TACCTCACTTGTGAGTCCACAGCTGGAGGTAACCTGCCAGCAGCCAGGCACA CCTCTCTCAAAGTTGACTTCAACAGTGGCCGAAAATCCAACAGAAAGAAATATG TGAAAACCAGTAAGTTGTAGCTTTGATAGGATTCAACCTACTAAAGATTGTA TGAAAGATAAAATCAGAATTCCAGAAAGATCCAAAAGTGTCTGAACAGACTCAG CAGTGTACGGTATGAGAATCTGTAACAAGCCCTCAGCAGGCACTGCCAAAGCT TTCCAAAGGCCAGGCCACAGGGCACACAAAGAACCTCTAAGACCTACAAAATTAAA TCTACAGAAGTCTAACAGGAAATTCTCACTGGGTTCAATAAGAATCCAAGA AACAAAGACATTAGATAAGATAAAATCTAAAGCCAAGGAAACAAAAGAAATGATG ATAAGGGAGATCATACCTACCGGCTCATTAGTGTGTCAGCCATCTGGGAAGACTCT AAAGTCAGGCCATTATCTGATGCTCATGACTTGTGAGAAACAGATCTGGTCACT TACGATGATATGGGGTAGGTACCTGGAGGCCAGATGCGAGGAGTAGGGGTT GCACTGGGTACATCTTTTACATGCAATGAGCTTGAAGAGATGTTGAAAAG AGAAGAGAAATGCCAGCTTAATGCAAGGAGTAGAGGGAGCCCTCAGAGGAATAA GAGGAACGTAACCTCTCTGGTACAGATCTGCCACTGTCACCTGATACCTCC TCCATGGGAAGGAAACTGTGAACCTTATCCAGAGATGAAATGCAATTAGTCTAGGAC CAAAGTCAAACAGAAACACTTAATGGGAGATCTGCATTCTAATCC | | |
| | ORF Start: ATG at 101 | ORF Stop: TAA at 2840 | |
| | SEQ ID NO: 340 | 913 aa | MW at 104046.0kD |
| NOV122a, CG59746-01 Protein Sequence | MAALFLRGFVQIGNCKTGISKSEAFIEAVERKKDKRLVLYFKSGKYSTFRSLNDNIQN VVLKSYRGNQNHLHLLTNNNNGLFIEGLSSTDAEQLKIFLDRVRHQNEVQPPVRPGKGG SVFSSTTQKEINKTSFHVKDEKSSSKSFEIAKGSGTGVILQRMPPLTSKLTITCGELSE NQHKKRKRMILSSSEMNEEFLKENNSVEYKKSFADCSCRCVSYNREKQLKLKELEENKK LECESSCIMNATGPNYLDDIGLLQALTEKMLVFLQQGYSDFGYTKWDKLKFELFP EYVYSGDRAFTIEKEPLAHLMTYIEDTSLCQFHHAGGKFAASGPCTLSKVDPQTVPENT | | |

ESVYSGDRAFTIEKEPLAHLMTYIEDTSLCQFHHAGGKFAASGPCTLSKVDPQTVPENT

| | |
|--|---|
| | KRKKYVKTSKFVAFDRIINPTKDLYEDKNIRI PERFQKVSEQTQQCDGMRICEQAPQQ ALPQSFPKPGTQGHTKNLLRPTKLNLQKSNRNSLLALGSNKNPRNKDILDKIJKAKE TKRNDDKGHDHTYRLISVSHLGKTLKSGHYICDAYDFEKQIWFTYDDMRVLGIQEAM QEDRRCTGYIFFYMHNEIFEMLKREENAQLNSKEVEETLQKE |
|--|---|

Further analysis of the NOV122a protein yielded the following properties shown in Table 122B.

| Table 122B. Protein Sequence Properties NOV122a | |
|--|---|
| PSort analysis: | 0.7000 probability located in nucleus; 0.4270 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1047 probability located in mitochondrial inner membrane |
| SignalP analysis: | Likely cleavage site between residues 16 and 17 |

A search of the NOV122a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 122C.

| Table 122C. Geneseq Results for NOV122a | | | | |
|--|--|----------------------------------|---|--------------|
| Geneseq Identifier | Protein/Organism/Length [Patent #, Date] | NOV122a Residues/ Match Residues | Identities/ Similarities for the Matched Region | Expect Value |
| AAU07888 | Polypeptide sequence for human hspG25 - Homo sapiens, 913 aa. [WO200166752-A2, 13-SEP-2001] | 1..913 1..913 | 913/913 (100%) 913/913 (100%) | 0.0 |
| AAB75607 | Human cancer associated antigen precursor HOM-TES-84/6 SEQ ID NO:6 - Homo sapiens, 912 aa. [WO200100874-A2, 04-JAN-2001] | 1..905 1..904 | 429/920 (46%) 566/920 (60%) | 0.0 |
| AAU07869 | Polypeptide sequence for mammalian Spg25 - Mammalia, 835 aa. [WO200166752-A2, 13-SEP-2001] | 1..904 1..834 | 335/921 (36%) 504/921 (54%) | e-147 |
| AAG75460 | Human colon cancer antigen protein SEQ ID NO:6224 - Homo sapiens, 109 aa. [WO200122920-A2, 05-APR-2001] | 810..912 3..107 | 61/105 (58%) 79/105 (75%) | 3e-28 |
| AAB39364 | Gene 8 human secreted protein homologous amino acid sequence | 810..871 1..64 | 39/64 (60%) 48/64 (74%) | 5e-15 |

In a BLAST search of public sequence databases, the NOV122a protein was found to have homology to the proteins shown in the BLASTP data in Table 122D.

| Table 122D. Public BLASTP Results for NOV122a | | | | |
|--|--|---|---|---------------------|
| Protein Accession Number | Protein/Organism/Length | NOV122a Residues/ Match Residues | Identities/ Similarities for the Matched Portion | Expect Value |
| Q9BXU7 | Ubiquitin carboxyl-terminal hydrolase 26 (EC 3.1.2.15) (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26) - Homo sapiens (Human), 913 aa. | 1..913 1..913 | 913/913 (100%) 913/913 (100%) | 0.0 |
| Q9HBJ7 | UBIQUITIN-SPECIFIC PROCESSING PROTEASE - Homo sapiens (Human), 922 aa. | 1..905 1..904 | 429/920 (46%) 566/920 (60%) | 0.0 |
| Q9HCH8 | KIAA1594 PROTEIN - Homo sapiens (Human), 931 aa (fragment). | 50..912 3..929 | 393/932 (42%) 535/932 (57%) | e-171 |
| Q99MX1 | Ubiquitin carboxyl-terminal hydrolase 26 (EC 3.1.2.15) (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26) - Mus musculus (Mouse), 835 aa. | 1..904 1..834 | 335/921 (36%) 504/921 (54%) | e-147 |
| Q9ES63 | UBIQUITIN-SPECIFIC PROCESSING PROTEASE - Mus musculus (Mouse), 869 aa. | 1..908 1..848 | 341/933 (36%) 480/933 (50%) | e-131 |

PFam analysis predicts that the NOV122a protein contains the domains shown in the Table 122E.

| Table 122E. Domain Analysis of NOV122a | | | |
|---|-----------------------------|--|---------------------|
| Pfam Domain | NOV122a Match Region | Identities/ Similarities for the Matched Region | Expect Value |
| UCH-1: domain 1 of 1 | 295..326 | 21/32 (66%) 29/32 (91%) | 8.8e-12 |

Example 123.

The NOV123 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 123A.

Table 123A. NOV123 Sequence Analysis

| | SEQ ID NO: 341 | 2146 bp |
|---|--|------------------------|
| NOV123a, CG88613-01 DNA Sequence | <p>GAAGGAGCGGGCATGAGGCCTGCCGTGCGGTGGAGCCTGAACGAGGGGAGGCC GGGCGCTGCCCGCGCCGCATGGACTGGAGGCCGCCAGGGGCCGCCGCC GCAGCCGGGACAGCAGCAGCACCTGGCCCGGCAGGGGCCGCCGCC GGGGCGGCCCTGGCCCGACAGAGGGTCCAGCCTCACAGCGAGCCTGAGAGGG CCGCCCTCGGGCTGCCCGACAGAGACTCCAGGAGAAATCTGACAGACAGG ACAGACTGAGGCCGCCAGCTGGCTTGAGTAGAGACCGAGAGGCCAACAGAAAAG ACGGAGCCAGACAGCTCCAGCTCCGGACGCATCTGAATGGACTGGTCAGAGCTGG AGACGACTTGTCTTGGACGGAGACGGGACAGATGGCCTTGGACTGATCCGACAG GTCCGACCTCCAGTTCAAGCCCAGGAGGCCAGCCCCCTGGACACAGCCAGGGTTCAT CGGCCCTGGACAGACGCTGGAAACGCATGGTCACAGACTCAGCCAGAGAGGGTCAACT CCTGGGCTGATAACCTCTGGACCCACAGAACAGTCTCCAGCCTCAGACTCACCCAGA AGGAGCTGTCCCTCAAAGAGCCAAGTGTGATGGCTCTGGAAAGAAATTGTATACT GATGGCTCAGGACACAACAGGATATTGAAGGTCCCTGGACAGAGCCATATACTGATG GCTCCAGAAAAAACAGGATACTGAAGCAGCCAGGAAACAGCCTGGCACTGGTGGTT CCAAATACAACAGGATACTGATGGCTCTGGACACAACCCAGACTGACGGTTCCAG ACAGCACCTGGGACAGACTGCTCTGGGAGAGCCTGAGGATGGCCCATTAAGGAAAC CAGAGCTGGAGAATTGCTGACTCACCTGACTCTCACCTGAAGTGTAGCCCCCTGTG CCTGTGCCCCGCCATCATTAACCCCTGAGACCCCTGAGGCTGAGGCCAGGCTG GGACCCCCCTCCGGGTTGAGGGGGCAGCGCGGCTTCTCCTCTGCCTCTTTCG ACGAGTCTGAGGATGACGTGTTGGCGGGGGCGAGGTGCAAGCGATCCGAGGACAG GTCCTGGGAGCAACCCCTGGAAGAAGCTGAAGACAGTCTGAAGTATTCAACCTTGTG GTCTCCTGGAAACACTACCTGGCTGACTCACCTGACTCTCACCTGAAGTGTAGCCCCCTGTG AGGCAAGAGAGGATGGTGGATCTGAACAGTGTCTGTGAGCAGGCCAGCCT GGAGCACTGATGAAAGACCCCTGCGACCTTCTGCTGCCTACTATGGCATGGT CTGCAAGGAGATGCCAGACCTCAACCAGATGGAAGACCTCTGGCTGACTTGAGGGCC CCTCATTATGGACTGCAAGATGGGAGCAGGACCTATCTGAAGAGGAGCTAGTGA GGCACGGGAAACGTCGGCCCGAGGACATGTGATGGAAAGATGGCTGTGGAC CCTGGGGCCCTACCTGGAGGAGCATGCCAGGTGCACTGACCAAGCCCCGCTACA TGCAGTGGAGGGAAACCATGAGCTCACCTCACCTGGGCTCCGGATGGGCA CAAGAAGGAGATGGGACCTGTAACACCAACTCAAGAAGACGCAAGCACTGGAGCAG GTGACAAAAGTGTGGAGGACTCTGTTGAGTGGAGACACGTCATCTGCAAAAGTAC TGGCATGCCAGAAAGAAACTCTGTGAAGCTCTGGAGATCTCCCTTCTTCAAGACCCA CGAGGTGGTAGGCAGCTCCCTCTTGTGCAAGCACACCGGCTGGCAAGGTC TGGATGATGAGACTTGGCAAGACGGTGGCTTGCCCAGCACAGCTAGCCACA GGCTGCCCCGGCTGAGGGCAACCGTGAAGGACGGCTACCTCTGGGCTGGACAACAT GATGTGCTCCTGAGGGCTGGCACAGAGCTGAGTGTCTAGCCACCATCAGGTTAA TTGGATGGCGGCACTGGCTGGAGGAGCCCTGAGATGGCATGGAGGCTGAGGTTG </p> | |
| | ORF Start: ATG at 13 | ORF Stop: TGA at 2062 |
| | SEQ ID NO: 342 | 683 aa MW at 75206.8kD |
| NOV123a, CG88613-01 Protein Sequence | <p>MRRCPGRGLSNEAAGALPAARMGLEPRGGRRRQPGQQRPQPGAGAPAGRPEGGGP WARTEGSSLHSEPERAGLGPAPGTEPSQAEFWTDQCQEPAAGLGVETERPKQKTEPD RSSLRTHLEWSWELETTICLWTETGTGDLWTDPHRSIDLQFPPEEASPWTQPGVHGPWT ELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKEPSADGSWKEYLTDGSR TQQDIECPWPTEPYTDGSQKKQDTEAARKQPGTGGFQIQQDTDGSWTQPSTDGSQTAPG TDCLLGEPEPDGPLEFPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKLLKTVLKYSFVVFSFR KHYPWVQLSGHAGNFQAGEDGRILKRFQCQCEQRSLEQLMKDPLRPFVAYYGMVLQDG QTFNQMEDLLADFECPSIMDCMGSRTYLEEELVKARERPRPRKDMDYEKMVAVDPGAP TPEEHQAQGVTKPRYMQWRETMSSSTLGFRIEGIKKADGTCTNFKKTQALEQVTKV LEDFVGDHVILQKVACLEELREALEISPFFKTHEVVGSSLFVHDHTGLAKVWMID FGKTVVALPDHQTLHSRLPWAEGNRREDGYLWG LDNMICL LQGLAQS </p> | |

Table 123A analysis of the NOV123 protein yielded the following properties shown in

| Table 123B. Protein Sequence Properties NOV123a | |
|--|---|
| PSort analysis: | 0.5663 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen) |
| SignalP analysis: | No Known Signal Sequence Predicted |

A search of the NOV123a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 123C.

| Table 123C. Geneseq Results for NOV123a | | | | |
|--|--|--|---|---------------------|
| Geneseq Identifier | Protein/Organism/Length [Patent #, Date] | NOV123a Residues/Match Residues | Identities/Similarities for the Matched Region | Expect Value |
| AAM41393 | Human polypeptide SEQ ID NO 6324 - Homo sapiens, 687 aa. [WO200153312-A1, 26-JUL-2001] | 1..683 5..687 | 682/683 (99%) 682/683 (99%) | 0.0 |
| AAM39607 | Human polypeptide SEQ ID NO 2752 - Homo sapiens, 711 aa. [WO200153312-A1, 26-JUL-2001] | 12..683 36..711 | 642/680 (94%) 643/680 (94%) | 0.0 |
| AAE04364 | Human kinase (PKIN)-5 - Homo sapiens, 798 aa. [WO200146397-A2, 28-JUN-2001] | 273..682 380..793 | 219/432 (50%) 285/432 (65%) | e-117 |

In a BLAST search of public sequence databases, the NOV123a protein was found to have homology to the proteins shown in the BLASTP data in Table 123D.

| Table 123D. Public BLASTP Results for NOV123a | | | | |
|--|---|--|--|---------------------|
| Protein Accession Number | Protein/Organism/Length | NOV123a Residues/Match Residues | Identities/Similarities for the Matched Portion | Expect Value |
| Q96DU7 | INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE C - | 1..683 1..683 | 683/683 (100%) 683/683 (100%) | 0.0 |

| | | | |
|--------|---|------------------|----------------------------------|
| Q96DU7 | INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE C - | 1..683 1..683 | 683/683 (100%) 683/683 (100%) |
| | | 4..604 | 601/601 (100%) |

| | | | | |
|----------|---|----------------------|--------------------------------|-------|
| | ISOENZYME (EC 2.7.1.127) - Homo sapiens (Human), 604 aa (fragment). | | | |
| S17682 | 1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - human, 472 aa. | 273..682 54..467 | 219/432 (50%) 285/432 (65%) | e-117 |
| CAB65055 | INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE B - Homo sapiens (Human), 946 aa. | 273..682 528..941 | 219/432 (50%) 285/432 (65%) | e-117 |
| Q96JS1 | INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE, ISOFORM B (EC 2.7.1.127) - Homo sapiens (Human), 946 aa. | 273..682 528..941 | 219/432 (50%) 285/432 (65%) | e-117 |

PFam analysis predicts that the NOV123a protein contains the domains shown in the Table 123E.

| Table 123E. Domain Analysis of NOV123a | | | |
|---|----------------------|---|--------------|
| Pfam Domain | NOV123a Match Region | Identities/ Similarities for the Matched Region | Expect Value |
| No Significant Matches Found | | | |

Example 124.

The NOV124 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 124A.

| Table 124A. NOV124 Sequence Analysis | |
|---|---|
| | SEQ ID NO: 343 1395 bp |
| NOV124a, CG59993-01 DNA Sequence | <pre> GGTAAGACGACCTCTGGATGCTCACCTGCCCTTCAACCTCTCGCCCCAGCTGTTT CCTCTGCCACCATGAGGAACATTTCAGAGAGAACCCAGGAGCTATTGTGGCTCCCTGC CACCACCCGCCACCGATGCCATTGACCCCTGSAJAACTCCACTGAGAATGGGGGT GCTGGGAGAGGCCAGGAGGACATGTTGCCAAACTGAAGGAGAAAGTTATTCAATGAGA TAAACAAGATTCCCTTACCAACCTGGCACTGATCGCATTGCTGTGGTTCTGGGCT CCTGCTCTCACCTGCTGCTTCATGCAAGAAATGCTGCTGCAAGAAGAAGAAG AACAAAGAAGGAGAAGGGCAAAGGCATGAAGAATGCCATGAACATGAAGGACATGAAAG GGGTCAGGATGAGGACGACGGCAGAGACAGGCCCTGACTGAGGGGAAGGTTAAGGGGA GGAGGGAAAAGAGGAGAACCTGGGCAAACCTGGCAGTTTCCCTGGACTATGATTTC CAGGCTAATCAGCTTACTGTGGCTTCTGCAAGGCTGCTGAACCTGCCCTGGACA TGGGAGGCACCTCAGACCCCTATGTCAAGGCTTCCCTCCCTGACAAGAAGAAGA ATATGAGACCAAAGTCCATGGAAAGACACTGAACCCGCCCTCAATGAAACCTTCACC TTCAAGGTGCCATACCAGGAGCTTGGGGCAAAACTCTGGTATGCCATCTATGACT TTGACCGCTTCTCCAAACATGACATCATTGGAGAGGTAAAGGTGCCTATGAACACAGT GGACCTCGGCCAGCCCATTGAGGAGTGGAGAGACCTGCAASGGGGAAAAGGAGGAG </pre> |

| | | | | | |
|---|---|---------|-----------------|--|--|
| | ACTCGCTCAAGCTGAGGGAGGTGGATGCACTCCTGGGCAAGAACAGTAGACAGC AGCGGCTGGACCCACACCTTCACGGACACTGACAAGATCCAGAGCTATCAATACC TCA | | | | |
| | ORF Start: ATG at 70 ORF Stop: TAG at 1327 | | | | |
| | SEQ ID NO: 344 | 419 aa | MW at 46871.8kD | | |
| NOV124a, CG59993-01 Protein Sequence | MRNIFKRNQEPIVAPATTATMPIGPVDNSTESGGAGESQEDMFAKLKEKLFNEINKI PLPPWALIAIAAVVAGLLLLTCCFCICKKCCCCKKNNKEKGKGMKNAMNMKDMKGQD DDDAETGLTEGEGEEEKEPENLGKLQFSLDYDFQANQLTVGVLQAELPALDMGGT SDPYVKVFLLPDKKKYETKVRKTLNPNAFNETFTFKVVPYQELGGKTLVMAIYDFDRF SKHDIIGEVKVPMTVDLGQPIEWRDLQGGEKEEPEKLGDICTSRLRYVPTAGKLTV ILEAKNLKMKMDVGLSDPVKIHLMQNGKRLKKKTTVKKTLNPYFNEFSFEIPFE QIQKVQVVVTVDYDKLGKNEAIGKIFVGNSATGTELRHWSMLANPRRPIAQWHSLK PEEEVDALLGKNA | | | | |
| | SEQ ID NO: 345 | 1338 bp | | | |
| NOV124b, CG59993-02 DNA Sequence | CCACCATGAGGAACATTTCAAGAGGAACCAAGGGCTATTGGCTCTGCCACAC CACCCGCACGATCCCATTGGACCCCTGGACAACACTCCACTGAGAGTGGGGGTCTGGG GAGAGTCAGGAGGACATGTTGCCAAACTGAAGGAGAAGTTATTCAATGAGATAAAC AGATTCCCTTACACCCCTGGCACTGATGCCATTGCTGTGTTGCTGGCTCCTGCT TCTCACCTGCTCTTCATGCCATTGCAAGAAATGCTGCTGCAAGAAGAAGAAGAACAAAG AAGGAGAAGGGCAAAGGTATGAGAAATGCCATGAACATGAAGGACATGAAGGGGTC AGGATGACGACGACGAGACAGGCTGACTGAGGGGAAGGTGAAGGGGAGGAGGA GAAAGAGCCAGAGAACCTGGCAAACACTGCAAGTTTCCCTGGACTATGATTTCAAGGCT AATCAGCTTACTGTGGCGTCTGCAGGCTGTAACCTGCCCTGGACATGGGAG GCACCTAGACCTTAAATGCTCAAGGTCTCTCCCTTCATGCAAGAAGAAGAACATATG GACCAAAGTCCATCGGAAGACATGAAACCTGCTTCAATGAAACCTTCACCTTCAAG GTGCCATACCGAGGCTTGGGGCAAACCTCTGGTATGCCATCTATGACTTTCACC GCTTCTCAAACATGACATCATGGAGAGGTAAGGTGCTATGAACACAGTGGACT CGGCAGGCCATTGAGGAGTGGAGAGACCTGCAAGCGGGAAAAGGAGGAGCCGGAG AAGCTGGCGACATCTGACCTCCCTGGCTATGCCCCACGGCGGGAAAGCTCACTG TCTGCATCTGGAGGCTAAGAACCTCAAGAAGATGGACGCTGGCGGGCTTTCAGACCC GTACGTGAAGATCCACTGATGCAAGAAGGGCTCAAGAAGAAGAACAAACC ATGAAGAAGAACCCCTGAACCCATACTTCAACGAGTCCTTCAGCTTGAGATCCCT TCGAGCAGATTCAAGAAAGTCCAGGTAGTGGTCACCGTGCTGGACTATGACAAGCTGG CAAGAAGCAAGCCATAGGAAGATCTCTGTGGGAGCAATGCCACGGCACAGAGCTG CGGCACTGGTCCGACATGCTGGCCAACCCCCGGAGGCCATGCCAGTGGCACTCGC TCAAGCCTGAGGAGGAGGAGGTGGTCACTCTGGCAAGAACAGTAGACAGCAGCGC TGGACCCACACCTTCACGGACACTGACAAGATCCAGAGCTATAAGGTCTAG GGCG | | | | |
| | ORF Start: ATG at 6 ORF Stop: TAG at 1263 | | | | |
| | SEQ ID NO: 346 | 419 aa | MW at 46845.9kD | | |
| NOV124b, CG59993-02 Protein Sequence | MRNIFKRNQEPIVAPATTATMPIGPVDNSTESGGAGESQEDMFAKLKEKLFNEINKI PLPPWALIAIAAVVAGLLLLTCCFCICKKCCCCKKNNKEKGKGMKNAMNMKDMKGQD DDDAETGLTEGEGEEEKEPENLGKLQFSLDYDFQANQLTVGVLQAELPALDMGGT SDPYVKVFLLPDKKKYETKVRKTLNPNAFNETFTFKVVPYQELGGKTLVMAIYDFDRF SKHDIIGEVKVPMTVDLGQPIEWRDLQGGEKEEPEKLGDICTSRLRYVPTAGKLTV ILEAKNLKMKMDVGLSDPVKIHLMQNGKRLKKKTTVKKTLNPYFNEFSFEIPFE QIQKVQVVVTVDYDKLGKNEAIGKIFVGNSATGTELRHWSMLANPRRPIAQWHSLK PEEEVGALLGKNA | | | | |

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 124B.

Table 124B. Comparison of NOV124a against NOV124b.

| Protein Sequence | NOV124a Residues/ Match Residues | Identities/ Similarities for the Matched Region |
|------------------|-------------------------------------|--|
| | | |

Further analysis of the NOV124a protein yielded the following properties shown in Table 124C.

| Table 124C. Protein Sequence Properties NOV124a | |
|--|--|
| PSort analysis: | 0.8202 probability located in mitochondrial inner membrane; 0.6000 probability located in endoplasmic reticulum (membrane); 0.3500 probability located in nucleus; 0.3034 probability located in mitochondrial intermembrane space |
| SignalP analysis: | No Known Signal Sequence Predicted |

A search of the NOV124a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 124D.

| Table 124D. Geneseq Results for NOV124a | | | | |
|--|---|---|--|---------------------|
| Geneseq Identifier | Protein/Organism/Length [Patent #, Date] | NOV124a Residues/ Match Residues | Identities/ Similarities for the Matched Region | Expect Value |
| AAR97722 | Mouse inositol polyphosphate binding protein IP4-BP - Mus musculus, 422 aa. [JP08092290-A, 09-APR-1996] | 1..419 1..422 | 412/422 (97%) 414/422 (97%) | 0.0 |
| AAU19715 | Human novel extracellular matrix protein, Seq ID No 365 - Homo sapiens, 461 aa. [WO200155368-A1, 02-AUG-2001] | 128..405 169..447 | 141/280 (50%) 201/280 (71%) | 2e-80 |
| AAU19714 | Human novel extracellular matrix protein, Seq ID No 364 - Homo sapiens, 295 aa. [WO200155368-A1, 02-AUG-2001] | 141..409 11..281 | 140/273 (51%) 193/273 (70%) | 3e-74 |
| AAW87702 | A human membrane fusion protein designated SYTAX2 - Homo sapiens, 375 aa. [WO9856813-A2, 17-DEC-1998] | 59..407 31..364 | 146/352 (41%) 220/352 (62%) | 4e-73 |
| AAO05534 | Human polypeptide SEQ ID NO 19426 - Homo sapiens, 149 aa. | 33..164 15..149 | 127/135 (94%) 131/135 (96%) | 5e-70 |

Upon BLASTP search of public sequence databases, the NOV124a protein was found to have homology to the proteins shown in the BLASTP data in Table 124E.

| Table 124E. Public BLASTP Results for NOV124a | | | | |
|--|---|--|--|---------------------|
| Protein Accession Number | Protein/Organism/Length | NOV124a Residues/Match Residues | Identities/Similarities for the Matched Portion | Expect Value |
| P29101 | Synaptotagmin II (SytII) - Rattus norvegicus (Rat), 422 aa. | 1..419 1..422 | 411/422 (97%) 414/422 (97%) | 0.0 |
| A55417 | synaptotagmin II - mouse, 422 aa. | 1..419 1..422 | 412/422 (97%) 414/422 (97%) | 0.0 |
| P46097 | Synaptotagmin II (SytII) - Mus musculus (Mouse), 422 aa. | 1..419 1..422 | 411/422 (97%) 413/422 (97%) | 0.0 |
| P24506 | Synaptotagmin B (Synaptic vesicle protein O-P65-B) - Discopyge ommata (Electric ray), 439 aa. | 10..419 27..439 | 341/413 (82%) 366/413 (88%) | 0.0 |
| P46096 | Synaptotagmin I (SytI) (p65) - Mus musculus (Mouse), 421 aa. | 10..419 8..421 | 323/418 (77%) 353/418 (84%) | 0.0 |

PFam analysis predicts that the NOV124a protein contains the domains shown in the Table 124F.

| Table 124F. Domain Analysis of NOV124a | | | |
|---|-----------------------------|---|---------------------|
| Pfam Domain | NOV124a Match Region | Identities/Similarities for the Matched Region | Expect Value |
| Adeno_E3_CR2: domain 1 of 1 | 62..108 | 16/50 (32%) 26/50 (52%) | 6.5 |
| C2: domain 1 of 2 | 156..242 | 54/97 (56%) 81/97 (84%) | 1.8e-42 |
| C2: domain 2 of 2 | 287..375 | 44/97 (45%) 80/97 (82%) | 2.9e-39 |

Example 125.

The NOV125 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 125A.

Table 125A. NOV125 Sequence Analysis

| | | |
|--|----------------|---------|
| | SEQ ID NO: 347 | 3226 bp |
|--|----------------|---------|

| | | | | |
|---|--|---------|------------------|--|
| NOV125a, CG59991-01 DNA Sequence | GGACCACTTCTGATCTCTGGTCCAACTACTTCACTGCAAGGCCGAAACA GGGGGGCCAGATGGACCCCCATTAGCACAGAGAGACGTCCACACTCTGTGAGCCC AAAGGGAGAAGGCTCAGGCCACGGCAGAGACGGAACCGAAAAGTCACGAAAAAC GCCTCAAGTTGCCAGTCCCTGCAGGAACAGACAGGCCCTGGGCCGCCCCACCTGG CTCAGAGCTTGGCTGCATGGGGTGAACATGGACTACAAGAGTCACGTGATGACC AAATTGGCTGAGGAGGGAGTGTACGTGCTGTTGAAACACTGCTGACTGGC CGGAAATGCAAACCTGGCTGGCTTGTGTTGATTCAGACGGTGGGGCTTCCGGCCTG CACGGTGTTCTGCACGGAAGTCAGGAATTGGAAATGGCTTAGCCAGAAGGATC GTGCTGCTGGCGCAAGGTTGACTCTACCAAGGAAATGTTCTCTACGTCTCTTCC TCCCCTTAGAGAGATGCAGCGGAAGAAGGAGGAGCTGTACAGAGTTCATCTCCAG GGAGTGGCCAGACTCCAGGCTCCGGTACGGAGGATCATGTCGGACCCAGGAAAGGCTG TTGTTCATATTGACGGTTGATGACCTGGCTCTGCTCTAACAAATGACACAAAGC TCTGCAAAAGACTGGCTGAGAAGCAGCTCCCTCACCTCTACGCAGTGTGAG GAAGGTCTGCTCTTGAGTCCTCTGATGTCACCGTCAGAGACGTGGCACAGAG AAAGCTCAAGTCAGAGTCGTGTCCTCCCGTACCTGTTAGTTAGAGGAATCTCCGGG AACAAAAGAATCCACTGCTCTTGAGCGGGGATTGGTACGATCAGAACACAAAGG GTTGCGTGCATGACAAACCGTGCAGCTGTCGACCCAGTGCAGGTGGCCGCGT GGCTCTCATCTGCTGGCCCTGCAGCTGCAGGACGGTGGGGAGAGCGTGC CCTCAACCAAACGCTCACAGGCTGACGCCGTTTGTGTTCATCGTCACCC TCGAGGCGTGGCTCCGGCCTGTCATACTGGAGGAAAGAGTTGCTCTGAAGCGCTTC TGCGTATGGCTGAGGGAGTGTGGAATAGGAACTCAGTGTGACGGTGACGAC TCATGGTTCAAGGACTCGGGAGTGTGACCTCCGCTCTGTTACATGAACATCT TCTCCAGAGACGGACTCTGAGGACTACACCTCTTCACCTCAGTCAGGAC TTCTGTCGGCCTTGTACTACGTTAGAGGCCCTGAAATCGAGCCAGCTCT CTCTGTACGTTGAGAAGACAAAGAGGCTCATGGAGCTTAAACAGGCAGGCTTCCAT CCACTCGCTTGGATGAAGCCTTCTGTTGGCCTGTCAGGAGAAGCAGCTTCAAGGAGG CCACTGGAGGTCTGCTGGCTGTGGCTGCCCCCTCCCTGGGGTGAAGCAGAAGCTTCTG ACTGGGCTCTCTGTTGGCTGAGCAGCTAATGCUAACUCCUAGGAGAACCCUTG CCCTCCACTGTGCTTCCGACTCAAGAACAGGTTGCTGAAATCGAGCCAGCTCT AGCTTCAAGAAGTGTGGCTTCCGATTAACCGAACCTGGACTGATGAGCATCT TCTGCCTCCAGCAGTGTGCGTATTGCGGAAATTGCGGTTGATGTCAAAGGGATCTT CCCAAGAGATGAGTCGCTGAGGCATGTCCTGTTGTCCTCTATGGATGCCGATAAG ACCCATTGAGGAGCAGTGGGAAGATTCTGCTCATGCTGGCACCCACCCAC TGGCGCAGCTGGACCTGGCAGCAGCATCTGACAGCGGGCCATGAAGACCCCTGT TGCAAGCTGAGGATCCCACCTGCAAGATCACGACCCCTGATGTTAGAAATGACAG ATTACCCCTGGTGTGAGCACCTCTGGAGAATGTCATGGCAACCGTAACCTAAGAT CCCTCAACTTGGAGGACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGC CTTAAACACCCAAAATGTTGGAGTCTTGGAGCTCTTGAGCTGATTGCTGTTGATTGAC CATGCGCTTACCTGAAAGATCTCCAAATTCACGACCTCCCCAGCCTGAAATCTC TGAGGCTGGCAGGAAACAAGGTGACAGACAGGAGGAAATGCTCTCAGTGTG GAGAGTCTCCAGTCGCCCCCTGCAAGCTGATACTGGAGGACTGTGGCATCACAGC ACGGGTTGCCAGACTCTGGCTCAGCCCTGTCAGCAACCCGGACTTGACACACCTG GCCTATCCAACAAAGCCTGGGAAGGCTGAAATCTACTGTGTCATCCATGAG GCTTCCCCTACTGAGTCGAGGAGCTGATGCTGAATCAGTGCACCTGGACACGGCT GGCTGTGGTTCTGACTTGGCTTATGGGTAACCTATGGCTGACGCACCTGAGCC TTAGCATGAACCTCTGGAAGACAATGGCTGAGCTTGTGCGAGGTCATGAGAGA ACCATCTGTATCTCCAGGACCTGGAGTGTGAAATGTCATCTCACCCCGCGTGC TGTGAGAGTCTGCTCTGTGATCTGAGGAGCAGACACCTGAAGAGCCTGGATCTC CGGACAATGCCCTGGTGAAGGCTGGGTTGCTGACTGTGCGAGGGACTGAAGCAAA GAACAGTGTCTGAGGACTCGGGTTGAAGGCTGAGACTGACTCTGATTGCTGT GAGGCACTCTCTGGCCCTTCTGCAACCCGACATGCAACGCTCTAAACCTGGTGC AGAATAACTCAGTCCAAAGGAATGATCAAGCTGTTGGCCTTGGCTGTC GTCTAACTTACAGATAATTGGCTGTTGAATGGCAGTACCCGTGCAAAATAAGGAAG CTGCTGGAGGAAGTGCAGCTACTCAAGCCCGAGTCGTAATTGACGGTAGTTGGCATT CTTTGATGAAGATGACCGGTACTGGTGGAAAAACTGAAGATAACGGAAACCTGCCCA CTCACACCCATCTGATGGAGGAACCTTAAACGCTGT | | | |
| | ORF Start: ATG at 69 ORF Stop: TGA at 3168 | | | |
| | SEQ ID NO: 348 | 1033 aa | MW at 116310.7kD | |
| NOV125a, CG59991-01 Protein Sequence | MGPPFSTRETSTLCEPKGRRLRPRQRNRQENVTNSLKLPGPLQEQTGLGPPHLGSEL LGHHGDWTDYKSHVMTKFAEEEDVRRSFNTAADWPEMQTLAGFDSDRWGFRPRTVV LHKGSGIGKSALARRIVLWCWAQGGLYQGMFYSVFFLPVREMQRKKESSVTEFISREW DSQAPVTEIMSRPERLFLIDFGDDLSVLNNDTTLCKDWAEKQPPTLIRSLLRKVL LPESFLIVTVRDVGTEKLKSEVVSPLYLLVRGISGEQRILLLERGIGEHQKTQGLRA IMNNRELLDQCQPVAVGSLICVALQLQDVVGESVAPFNQTLTGLHAASFVHQLTG VRCLNLEERVVLKRFCRMAVEGVWNRKSVFDGDDLMVQGLGESELRALFHMMNILLPD SHCEEYTFHLSQDFCAALYYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHIHSL WMKRFLPGLUSEDVRRPLFVLLGCPVPLGVFKQLLHWVSLLGQQPNATTGDTLDAPH | | | |

ALL INFORMATION CONTAINED HEREIN IS UNPUBLISHED PROPERTY OF THE GOVERNMENT OF THE UNITED STATES OF AMERICA.
IT IS PROVIDED PURSUANT TO A GOVERNMENT CONTRACT AND IS NOT TO BE DISCLOSED TO UNAUTHORIZED PERSONS
OR USED FOR OTHER THAN THE PURPOSES OF THE CONTRACT.

| | |
|--|---|
| | LTRLGLKACGLTSDCCEALSLALSNCNRHLTSNLVQNNFSPKGMMKLCSAFACPTSNL QIIGLWKWQYPVQIRKLLEEVQLLKPRVVIDGSWSHFDEDDRYWWKN |
|--|---|

Further analysis of the NOV125a protein yielded the following properties shown in Table 125B.

| Table 125B. Protein Sequence Properties NOV125a | |
|--|---|
| PSort analysis: | 0.7600 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen) |
| SignalP analysis: | No Known Signal Sequence Predicted |

A search of the NOV125a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 125C.

| Table 125C. Geneseq Results for NOV125a | | | | |
|--|---|----------------------------------|---|--------------|
| Geneseq Identifier | Protein/Organism/Length [Patent #, Date] | NOV125a Residues/ Match Residues | Identities/ Similarities for the Matched Region | Expect Value |
| AAE07514 | Human PYRIN-1 protein - Homo sapiens, 1034 aa. [WO200161005-A2, 23-AUG-2001] | 103..934 207..1003 | 276/843 (32%) 445/843 (52%) | e-126 |
| AAE07513 | Human nucleotide binding site 1 (NBS-1) protein - Homo sapiens, 1033 aa. [WO200161005-A2, 23-AUG-2001] | 114..935 180..990 | 281/839 (33%) 431/839 (50%) | e-120 |
| AAU07878 | Polypeptide sequence for mammalian Spg65 - Mammalia, 748 aa. [WO200166752-A2, 13-SEP-2001] | 207..963 9..748 | 218/766 (28%) 380/766 (49%) | 7e-95 |
| AAE06758 | Human G-protein coupled receptor-8 (GCREC-8) protein - Homo sapiens, 1473 aa. [WO200157085-A2, 09-AUG-2001] | 21..764 219..959 | 235/772 (30%) 380/772 (48%) | 3e-88 |
| AAB62571 | Human CARD-7 polypeptide - Homo | 21..764 | 235/772 (30%) | 3e-88 |

In a BLAST search of public sequence databases, the NOV125a protein was found to have homology to the proteins shown in the BLASTP data in Table 125D.

Table 125D. Public BLASTP Results for NOV125a

| Protein Accession Number | Protein/Organism/Length | NOV125a Residues/Match Residues | Identities/Similarities for the Matched Portion | Expect Value |
|--------------------------|--|---------------------------------|---|--------------|
| Q9JLR2 | MATERNAL-ANTIGEN-TATH-EMBRYOS-REQUIRE PROTEIN - Mus musculus (Mouse), 1111 aa. | 24..1033 104..1111 | 548/1019 (53%) 716/1019 (69%) | 0.0 |
| Q9R1M5 | MATER PROTEIN - Mus musculus (Mouse), 1111 aa. | 24..1033 104..1111 | 547/1019 (53%) 716/1019 (69%) | 0.0 |
| AAL35293 | NALP4 - Homo sapiens (Human), 994 aa. | 63..958 94..981 | 291/907 (32%) 473/907 (52%) | e-133 |
| Q96MN2 | CDNA FLJ32126 FIS, CLONE PEBLM2000112, WEAKLY SIMILAR TO HOMO SAPIENS NUCLEOTIDE-BINDING SITE PROTEIN 1 mRNA - Homo sapiens (Human), 919 aa. | 63..958 19..906 | 291/907 (32%) 473/907 (52%) | e-133 |
| AAL12497 | CRYOPYRIN - Homo sapiens (Human), 1034 aa. | 103..934 207..1003 | 276/843 (32%) 445/843 (52%) | e-125 |

PFam analysis predicts that the NOV125a protein contains the domains shown in the Table 125E.

Table 125E. Domain Analysis of NOV125a

| Pfam Domain | NOV125a Match Region | Identities/Similarities for the Matched Region | Expect Value |
|--------------------|----------------------|--|--------------|
| LRR: domain 1 of 6 | 671..695 | 6/25 (24%) 16/25 (64%) | 1.6e+02 |
| LRR: domain 2 of 6 | 728..752 | 7/27 (26%) 17/27 (63%) | 2.3e+02 |

| | | | |
|--------------------|----------|--|---------|
| LRR: domain 4 of 6 | 814..856 | | 4.3e+02 |
|--------------------|----------|--|---------|

| | | | |
|--------------------|----------|---------------------------|---------|
| | | 14/25 (56%) | |
| LRR: domain 5 of 6 | 899..923 | 8/26 (31%) 20/26 (77%) | 27 |
| LRR: domain 6 of 6 | 956..977 | 7/25 (28%) 16/25 (64%) | 2.9e+02 |

Example 126.

The NOV126 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 126A.

Table 126A. NOV126 Sequence Analysis

| Table 126A. NOV126 Sequence Analysis | | | |
|--------------------------------------|--|---------|-----------------------|
| | SEQ ID NO: 349 | 2310 bp | |
| NOV126a, CG59987-01 DNA Sequence | CCGGCCCTCAGTCGCCGTCCCCCTCCGGCCCCC3CGCCGCTAGCATGACCGACGCC TGTGCCC CGGGCCCCCAGCCGCTGGAGAAAGGAJAACGAGCGCTACTTTCGGAAGGG CTGTAATCCCCCTTGACAAACCCGGCCGGACTAAATTGAGAATCAAGAGCTGCTTTG AATCAGCAGATCTGAAAGCCGTGGGGATGAGGACCGGGAGCGGAAACCTCTGAAAG TGGCCACAACACTAAAGGTGGGGAGCAAGTGCCTGGAGCTGAGCTTCCTGCAACTC AGACCTCGAGATGCTCAAGGAAGAGCTGGAGGGCTGAACATCTCGTGGCCCTATG CAGAACACAGAGGAGGCAATTACGATTTCCCTGATTTCCCTTGGCCCTGAAGGAAACGA AAGACGTCGACTTTGCGACTGCTCAAGGATTATACCTGGAAACATTACAGTGAAGA TGGCTATTATATGAAGATGAAATTGAGATCTTATGGATCTGAGACAAGCTTGTGG ACGCCCTAGCCGGGATGAGGCCGGGGTGGAACTGCTGATGACATACTTCAGCTGG GCTTTGTGAGAGTGCATTCTCCGCCAACGGCAGATGGGACTCTGTTCACCTG GTATGACTCTCACCGGGGTTCCGGTCAGCGAGCAATCTGCTGCTGGAGAAGGGC AGTGTCTGTCAACACTGGGGCCCTACACCCAGATGGGACCCGGTGTATCGGC AGACG CAGGCTGGCTGGAGACTGCCATAGTGCCTTCAGAGAGGCCAGGGTTT AAATTACCTGAAAGACACATTACCCATACTCAAGTTACGACATGAGCCCTGCCATG CTCAGCGTCTCGTCAAATGATGCTTGCAAGGCCAAGAAGCGTGGTGGAGAAA TCAGCCTTCTGGATCTGGGAATGAAATTCTCATGCTGGTGAAGGGTGGCTCAGGAGG TGCTAAGGTGGGGAGGGTCAACACAGTCAACCCAGCAGCTGAGCCAGGCCGTG AAAGAGAACATCCCCACTCTTGGCCAGCTAGGCTGCTGGAGGCCACCACACTACG CGGCCCTGGCCCACTACTTCACTGCCATCCTCTCATGCCACCCAGGTGAAGCCAGG CACGGATCTGGACCACCAAGGAGAAGTGCCTGCTCCAGCTACGACCATGCCAGAG GGGCTGACACCCCTGGCCACACTGAAGAATGATGCCAGCAGGCCAGACGTGGGAGG CCCACCTTGCGCAGAGCATGGCTCATCACGAGGACTCGGTGGGGAGGCCCTG CAAGAACGTCGGAGCATTGAGGTGCTCACAGAGGGTGTGTGCGGCCAGGAACGC TCCCGCTCACGTACGCCACGCCAGCAGGAGGAGATGACCTGCTGAACCTGATGACG CCCCCAGACTGTTGTGCTAAACTGAGCAAGAGGTTGACATTATATTGCCCTG TCCAGCTGACAGTCACGGACTCTTCCAGAGACTGGGCCCTATGTGTGCTCGGCT AACAAAGGGTGGACGCCCTCTCGAAGCAGATCCGCTTCACTGAGCAAGAACGGGACTTG GGTCACCTTGAGGGAAACGCCCGGTTCAAGGTTCACTTCTGGATCTTACTGCTC TGCTCGGTGGCAGAGGCCGGAGGAGATTATATTGCTCCATTGAGCTTGTGGAT TGTAAGTGGCTGACGCTGAGTGGAGTTATGAAGCTGCTGAAGAGCTTGGCAGGAGC AGATCCAGATGAAAGTGTGAGCCTCTGGACTCCACATCATCATGCTAAAGAG TGCACACATACTCCGTGGGAATGAGAAAACACTTCCATGATGTGCTTGTG GATGAGCAGAACAAACTGATAAAACCAAGAAAATCTCAAGAACGTTCTCTCTGAGT GGGGCACCAACAAAGAACAGACAGAACAGTCAAGGAGCAGACCTTGTGCCCTCATGGTGG GGCTGACGGCCCTAGGTCAAGAAGAAGCTGCCCTCCCTTCAAGCTTCTCAACTC GACAGTTGGTACTAATGTGAGGAAACAAACATGTTCAAGGCCAGACATTTCCGG TGCTGACTCGGCCCTAAAGCTTGTGCCATAATGGAAAATCTATCTATCTGTCTC AAATCTGTCTTCTCATAGTGTAAACTCACATTGATGTGTTTTATGAAGGAAAGT AACCAAGAACCTCTAGGAATTAGTGAAGAAACTTTTGAGGTG | | |
| | ORF Start: ATG at 46 | | ORF Stop: TAA at 2104 |
| | SEQ ID NO: 350 | 686 aa | MW at 76812.3kD |
| NOV126a. | MTDALLPAAPQPLEKENDGYFRKGNCNPLAQTRGRSKLQNQRAALNQQLKAVRMRMTGAE | | |

| | | | |
|---|---|--|--|
| | EGDLGFTLRGNAAPVQVHFLDPYCSASVAGAREGDYIVSIQLVDCWKLTLEVMKLLKS FGEDEIEMKVVSLLDSTSSMHNKSATYSVGMQKTYSMICLAIIDDDKTDKKKISKKL SPLSWGTONKRQKSASTLCPLPSVGAARPQVKKLPSFFSLNSDSSWY | | |
| | SEQ ID NO: 351 2109 bp | | |
| NOV126b, CG59987-02 DNA Sequence | CGCCGCTAACCATGACCGACGCCGTGTCGCCCCGGCCCCCAGCCGCTGGAGAAGGAG AAGCACGCCACTTTCGGAGGCCGCTGTAATCCCCTTGACAAAACCGGCCGGAGTAAAT TGCAGAACATCAAAGAGCTGCTTGAATCAGCAGATCTGAAAGCCTGCGGATGAGGAC CGGAGCGAAAACCTCTGAAAGTGGCACAAACTCAAAGGTGCGGGAGCAAGTGCAG CTGGAGCTGAGCTTCGTCAAACTCAGACCTGCAAGATGCTCAAGGAAGAGCTGGAGGGC TGAACATCTCGGGCTGCTATCAGAACACAGAGGAGCATTACGATTCCCTGAT TCCCTTGGCTGAAGGAACCGAACAGCTGCACTTGCAGTCGTCCTCAAGGATTT ATCTTGAACATACAGTGAAGATGGTATTATATGAAGATGAAATTGAGATCTTA TGGATCTGAGACAAGCTTGTGCGACGCCGCTAGCGGAGTGGAGCGGGGTGAAACTGCT GATGACATACTTCATCAGCTGGCTTGTGAGAGTCGATITCTCCGGCCACACGG CAGATGGGACTCTTCACCTGTATGACTCTCACCAGGGTCCGGTCAGCCAGC AGAACCTGCTGCTGGAGAACGCCAGTGTCTGTTCAACACTGGGGCCCTACACCCA GATTGGGACCCGGTGCATGGCAGACGCAGGCTGGGCTGGAGAGTGCATAGATGCC TTTCAGAGAGCCGAGGGTTTAAATTACCTGAAAGACACATTACCCATACTCCAA GTTACGACATGAGCCCTGCCATGCTCGCAGCTGCTGTCGTCAAAATGATGCTTGACAAAGC CCAAGAAAGCGTTGAGAAAATCAGCTTCTGGATCCGGATGAAATTCTTCATG CTGGTGAAGGTGGCTCAGGAGCTGCTAACGGTGGAGAGGTCTACCAACAGCTACACG CAGCCATGAGCCAGGCGCCGTAAAGAGAACATCCCTACTCCTGGCCAGCTTAGC CTGCGTGAAGGCCACCACCTACCGCCCTGCCACTACTCACTGCCATCCTCCTC ATCGACCAACAGGTGAAGGCCAGCAGGATCTGGCACCCAGGAGAAGTGCCTGCTCC AGCTTACGACCATGCCAGGGGCTGACACCCCTGGCCACACTGAAGAATGATCA GCAGCGCCACAGCTGGGAAGTCCCATTGCGCAGGCCATGGCTCATCAGAGGAG TCGGTGGGGAGGAAGCCTGCAAGAAGCTGCGAGCATTGAGGTGCTACAGAAGG TGCTGTGCGCAGAGGAACGCTCCCGCTACGTACGCCAGCACCAGGAGGAGGA TGACCTGCTGAACTGTATCGACGCCCTGGAGTGTGCTAAACTGAGGAAGAGGTT GACATTATATTGCCCCAGTTCTCAAGCTGACAGTCACGGACTTCTCCAGAAGCATCCGCTT GCCCTTATCTGTTTGGCTACAAGCGTGGACGCCCTCTCGAAGGATCCGCTT CACTGAGAAAGGGACTGGGTTACCTTGAGAGGAAACCCCCCTCAGGTT CACTTCCTGGATCTTACTGCTCTGCCCTGGCAGGAGGCCGGAGGAGATTATA TTGTCTCATTCACTGTTGGGATGTAAGTGGCTGACGCTGACTGAGGTTATGAAGCT GCTGAAGAGCTTGGCGAGGAGAGTCAGATGAGAAGTCTGAGGCTTCTGGACTCC ACATCATCCATGCTATAAGACTGCCACATCTGGGAATGTAGAAAACGTA CCATGATCTGCTTACCCATTGATGATGACGACAAACTGATAAAACCAAGAAAATCTC CAAGAACCTTCTTCTGACTGGGGCACCACAAAGAACAGACAGAACAGTCA ACCTTGCCCTCCATCGGTGGGCTGCACGGCCTCAGGTCAAGAACAGTGCCTC CCCCCTTCAGCCTCTCAACTCAGACACTTGTACTAATGTGAGGAACAAACAT GTTCAAGCCCCGAACATTCTC | | |
| | ORF Start: ATG at 11 ORF Stop: TAG at 1844 | | |
| | SEQ ID NO: 352 611 aa MW at 68613.9kD | | |
| NOV126b, CG59987-02 Protein Sequence | MTDALLPAAPQPLEKENDGYFRKGNCPLAQGRSKLQNQRALNQQILKAVRMRTGAE NLKVATNSKVREQRVLELSFVNSDLQMLKEELEGLNISVGVYQNTTEAFTIPLIPLG LKETKDVFDFAVVLKDFILEHYSSEDGYLVEDEIAIDMLDLRQACRTPSRDEAGVELLMYT FIQLGFVESRFPPTTRQMGFLFTWYDSLTVPSVQSNLLLEKAQAVLFNTGALYTQIGT RCDRQTQAGLESIAIDAFQRAAGVLYNKDTFTHTPSYDMSPAMLSVLVKMMLAQAEQS VFEKISLPGIRNEFFMLVKVAQEAAKVGEVYQQLHAAMSQAPVKENIPYSWASLACVK AHHYAAALAHYFTAILLIDHQVKPGTDLDHQEKCLSQLYDHMPPEGLTPLATLKDQQR QLGKSHLRRAMAHHHEESVREALCKKLRSIEVLQVKLCAAQERSRLTYAQHQEEEDDLL NLIDAPSIVAKTEQEVDIILPQFSKLTVTDFQKLGPPLSVPSANKRWTPPRSIRFTAE EGDLGFTLRCNAPVQVHFLDPYCSASVAGAREGDYIVSIQLVDCWKWITISFVMKLIKS FGEDEIEMKVVSLLDSTSSMHNKSATYSVGM | | |

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 126B.

Table 126B. Comparison of NOV126a against NOV126b.

| Protein Sequence | NOV126a Residues/ Match Residues | Identities/ Similarities for the Matched Region |
|-------------------------|---|--|
| NOV126b | 1..611 1..611 | 585/612 (95%) 590/612 (95%) |
| | | |

Further analysis of the NOV126a protein yielded the following properties shown in Table 126C.

Table 126C. Protein Sequence Properties NOV126a

| | |
|-------------------|---|
| PSort analysis: | 0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen) |
| SignalP analysis: | No Known Signal Sequence Predicted |

A search of the NOV126a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 126D.

Table 126D. Geneseq Results for NOV126a

| Geneseq Identifier | Protein/Organism/Length [Patent #, Date] | NOV126a Residues/ Match Residues | Identities/ Similarities for the Matched Region | Expect Value |
|---------------------------|--|---|--|---------------------|
| AAU10192 | Human prostate specific protein PSL22 - Homo sapiens, 686 aa. [WO200172962-A2, 04-OCT-2001] | 1..686 1..686 | 660/687 (96%) 665/687 (96%) | 0.0 |
| AAB68561 | Human GTP-binding associated protein #61 - Homo sapiens, 666 aa. [WO200105970-A2, 25-JAN-2001] | 27..686 7..666 | 626/661 (94%) 633/661 (95%) | 0.0 |
| AAG64579 | Human transcription termination factor binding protein 54 - Homo sapiens, 488 aa [CN1297918-A, 06- | 201..686 3..488 | 458/487 (94%) 464/487 (95%) | 0.0 |

| | | | | |
|----------|---|--------------------|-------------------------------|-------|
| | [WO200063392-A1, 26-OCT-2000] | | | |
| AAU00869 | Human cancer related protein 5 - Homo sapiens, 257 aa. [WO200118014-A1, 15-MAR-2001] | 409..597 8..196 | 70/189 (37%) 102/189 (53%) | 2e-27 |

In a BLAST search of public sequence databases, the NOV126a protein was found to have homology to the proteins shown in the BLASTP data in Table 126E.

| Table 126E. Public BLASTP Results for NOV126a | | | | |
|---|---|---------------------------------|---|--------------|
| Protein Accession Number | Protein/Organism/Length | NOV126a Residues/Match Residues | Identities/Similarities for the Matched Portion | Expect Value |
| Q96RU1 | RHOPHILIN-LIKE PROTEIN - Homo sapiens (Human), 685 aa. | 1..686 1..685 | 627/688 (91%) 640/688 (92%) | 0.0 |
| Q9DBN2 | 1300002E07RIK PROTEIN - Mus musculus (Mouse), 686 aa. | 1..686 1..686 | 573/687 (83%) 616/687 (89%) | 0.0 |
| Q61085 | GTP-RHO binding protein 1 (Rhophilin) - Mus musculus (Mouse), 643 aa. | 16..596 20..580 | 273/583 (46%) 361/583 (61%) | e-135 |
| Q9XYY9 | RHOPHILIN - Drosophila melanogaster (Fruit fly), 718 aa. | 21..615 31..674 | 248/654 (37%) 363/654 (54%) | e-110 |
| Q96PV9 | KIAA1929 PROTEIN - Homo sapiens (Human), 410 aa (fragment). | 23..366 17..362 | 178/346 (51%) 241/346 (69%) | 1e-93 |

PFam analysis predicts that the NOV126a protein contains the domains shown in the Table 126F.

| Table 126F. Domain Analysis of NOV126a | | | |
|--|----------------------|--|--------------|
| Pfam Domain | NOV126a Match Region | Identities/Similarities for the Matched Region | Expect Value |
| HR1: domain 1 of 1 | 38..110 | 19/87 (22%) 53/87 (61%) | 1.2e-05 |
| BRO1: domain 1 of 1 | 111..263 | 60/172 (35%) | 3.8e-56 |

| | | | |
|-------------------|---------|---------------------------|-------|
| PDZ domain 1 of 1 | 13..598 | 0.84 (14%) 53.84 (63%) | 1e-05 |
|-------------------|---------|---------------------------|-------|

Example 127.

The NOV127 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 127A.

Table 127A. NOV127 Sequence Analysis

| | SEQ ID NO: 353 | 3351 bp |
|-------------------------------------|---|---------|
| NOV127a, CG59971-01 DNA Sequence | CCTCCCGTGGCCATGACGACCGCTCAGAGGGACTCCCTGTGAGCTGGGGGT TGCTGCGGAGTCGGTGTATGTCGTCCTGCTGAGCACCCCTGAGCTGAC TCCCACACTGCACACAGCTGAACCCACGTTAGCTGACCCCTGGGGCATGGGCC GGCCAGAACAGGCTTGTGGCTGCACCCATCTGCCGACTCCCTGTTATTCTC A3CTTCAGTTCTCTCGATGTCAGAAAACACTTCAGCTGGTCCATGTC TGTG3CTCTGGGCCACAGGGCCATCAAGGTTTCCACTGTCATGGCTCCAGGCA CTGGAG3CTCGAGGTGTTCCACTGTCATGGCTCCAGGCACTACTCCC A3CTGGAGACCCCTGATTGCAAGCAGGAGCTCCAGGCAATTAGAGGAGCTCTCAGC CTGCGCGGCGACTCTGCTGTCCTGCCCTGGCTGCTGCTTCTGCAACTTC A3CTACAATGCACTGACCGCTTAAGACAGCTCCCTGCCGCTTGTCAAGCTTGCGTT TCTGAAACCTAACGCCAAATCAAGTCCAGGACTGTCAAGGATTCTGATGGATTG T3AGCTCCACCATCTGACATCTCTATAATCGCTGCAATTGTCAGGAAATGGGA CCCTCAGGGCTGCTCTGGGGCTCTGATACTGCGAGGCAATGAGCTTGGAGCCTGC CAGGCCTAGAGCAGCTGAGGAATCTGCGCACCTGGATTGGCATACAACCTGCTGGA A9GACACUCCCCGGAGCCTGACCCACCTGGCTGTCAGGCTGCAAGCTTACCTG GAGGGAAACCTCTTGGTTGACCCCTGAGCACCGAGCAGCAGCCACTGCCAGTACTTGT CACCCCGGGCCAGGGATGCTGACTGGCTTCTTCGATGGCAAGGTTGTC GACAGATTTCAGCAGACTCACACATCTGGGGCTCAGCCCCATGGGCCACCTTTG CCCTGGCCAGTGGGAGTACTCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCC TCTCTCAGGGGGTGTGACCCAGCCCTGCTCATAAGTTAAGAGCCGAGTCCG TGTGAGGCGGGCAAGCATCTCTGAAACCTGAGGACTGATACTGGAACCCCGAACTCTG AACCCTCTCGGGCTGGTTGGTGTGCTGAGCAGCACCCGGAGCTGGAGCTCATGAGCA GTTTCCGGGAACGGTTGGCCCAAACGGCTGGCTGAGTACAGGAGTCACCTGGAGCCTC CGGAAACCTCTGGCCGCCCCACTACTCTGCAACCCAGTCACCTCCAGGCCAGC TCCAGGGCCCGACACTGCAACCCAGACCTCACCCCGCAGGAGGAAGCCAGAGGCC C3CAGGAGTCACACAGAAAAATGTCAGGAGGTCAGGGGGAGGAGCCACAGGAGGAGA AGAGGAGAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGA GAGGAGGAGGAGGAGGAGAAGAGGAGGAGGAGGAGGAGGAGGAG TCTGTCGCCCTGTGGTGTCCCCCTGGAGGGGCTGAGGGCGTACGGGGAGGGA ATGTTTCTCAGGGTCACTCTGCCACCTGTTGAGGTGAACTCCAAGCAGCTCG ACCTGGAGCAGCTGGAGCTCAGAGCTGGAGGAGCTGAGATAGAGCCGGAGGCC AGGGCCAGGGCTCCCTCTGCGCAGGGCTCAGATCTGCTCCCTGGAGGCC CCTCAGTCTGCGCTCTCCTACATCTGCTGCACTGGCAAGGGCTGCGTATTG CTGAGGCTGATGCCACGCACTGTCAGGAGCTGCTTGGCTGTGACCCAGTC CTAATGTGGCTGGGAACAGCTGGGGAGGCCAGGGACCTCTGCTGGTAGATTCCA GTGTCTACGCTGTGGCCATGAGTTCAAGCCAGGGAGGCCAGGATGGGATTAGACAGT GAGGAAGCTGGAGGCTCTGCAAAAGACAGAACTCTGCTGTTGTC GTGGTAGTGTGACCATGGTCTCTGCGTGTCTGGGGAAACCCCAACAGGGAGCG GAAACAGGGAGGAGCAGTCTGGCTCTCTGGCTGCAAGGCTGTCTGCC CTGGCCATGGTACCCAGGACCTTGACAGGGCAAGAACAGCCACCTCAGGACCGAGCA CCCGTGACCATGGTAGTTGGAGGCTCAGTCCGCCCTGAGCGCTGTGGCTCGC T3TGGACCAACGACTGGGCTCTGCAAGGAGGCTCTGGAGGTCTCAGCAGGCCAGGAG GAGTTCAGTGTGCTCAAGTGGCATTGGCAAGCCACACTGGGGAGTTCA T3TGGCTTGTGGTGTGCTGAGCTGGCTGAGGCTGAGGAGGAGGAG GAGTGAGCTCCAGTAGCTGCTGAGCTGAGGCTGAGGAGGAGGAG AGTGGCATAGAGCTGGGCTGAGGAGGCCCTGGGGCTAGAGTGGGAGCTGGGG GGGGCCGCTGTGCTGCTGAGGAGGCTGAGGAGGAGGAGGAGGAG GCTCTTGTGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAG GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG TGGAGGCTGGCCAGTCTCTACCTTGCGGCTCTGGTTGAAAGGTGAAGCCTCTG GCAAGCTGATGCTCCCTCACCTGCGCTGATCCCTGTTGCTGACTCCGTCACCC TTCTCTTAGATGAGGATGCTGAGGCTCCCGGAGAGCCCTCTCCAGCAGCAT CTGGCGAACCCCTGAGAAGGCTCCCTGGGGGGGGGCGCCCTGCTGCGTGTG GGAGCAGGAGCCACTGAGAAGCTGAGGCTCCGCTGCTGACTACCGCTCAGGCC GACTTGCGGCTGCTCTACCATGAGGAGGCTGAGGAGGAGCTTGGGACTCC GTGTTGTGTCAGGAGCAGCTGACAGCCCTGCTGCGTGGATCCGGGAACCATGGGA | |

| SEQ ID NO: 354 | 398 aa | MW at 42104 kD |
|----------------|---|----------------|
| NOV127a, | MTIAQRDLSLWKASLMEESRDUVLSGCGSTISMXTPTIQQINHVFEIHLIGFWBPGQTG | |

| | | |
|-------------------------------------|--|---------|
| CG59971-01 Protein Sequence | FVALPSHPADSPVILQLQFLFDVLQKTLISLKLHVAGPGPTGPIKIFPFKSLRHLELRA GVPLHCLHLRGIVSOLETLICRSLSQALEELLSACGGDFCSALPWALLSANFSYNA LTALDSSLRLSALSRLFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGS AIGVLILRGNEELRSLPGLQEQLRNRLRHLDDAYNLLEGHRELSPLWLLAELRKLYLEGNP LWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSTLDFQQTHTSLGLSPMGPPLPWPV GSTPETSGGPDLSDLSSGGVVVTQPLLHKVSRVRVRASISEPSPDTPEPRTLNPS AGWFVQQHPELEMSFRERFGRNWLQYRSHLEPSGNLPATPTTSAPSAPASSQGP DTAPRSPSPQEEARCPQESPQKMSEEVRAEPEQEEEEKEGKEEKGEMVEQ3EEEAG EEEEEEQDQKEVEAEICRPLLVCPLEGPEGVGRRECFLRVTS AHLFEVELQAARTLER LELQSLEAAEIPEAQAAQGPPLAAGQSDLLPGAPILSLRFSYICPDRQLRRYLVLLEPD AHAQAVQELLAVLPTVNTNAREQLGGEARDLLLGRFQCLRCRGHEFKPEEPRMGLOSEEGW RPLFQKTESPAVCNCSDHVLLAVSRGTPNRERKQGEGQSLAPSPSASPVCCHPPGHG DHLDRAKNSPPQAPSTRDHGSWLSLSPARCGLRSVDRLLRFLDVEVFDSAQEEFQC CLKVPMALAGHTGEFMCLVVVSDRRLYLLKVTGEMSEPPASLQLTLAVPLQDLSGIE LGLAGQSLRLEWAAGAGRCVLLPRDARHCRAFLELLGLVLSLPPAWRNCSVATEEEV TPQHRLWPLLEKDSLEARQFYLRAFLVEGEASVQLMLPSTCLVSLLLTSTLFLLD EDAAGSPAEPSPAASEKVPVPPGPAVRVREQQPLSSLSVLLYRASAEDLRL LFYDEVSRLESFWALRVVCQEQTLALLWIREPWEELFSIGRTVIQEALALDR | |
| | SEQ ID NO: 355 | 3348 bp |
| NOV127b, CG59971-02 DNA Sequence | CGTCCCCTGGCCATGACGCCGCTCAGAGGGACTCCCTGTTGGAAGCTCGGGGGT TGCTCGGGAGTCGGTGTGTTGGCTCTGCTGCTGAGCACCTGGGCCATGGGCCCT TCCACACTGCAACAGCTGAACACAGTATTGAGCTGCACCTGGGCCATGGGCCCT GGCAGACAGGCTTGTGGCTCTGCCCTCCATCTGCCGACTCCCCCTGTTATTCTC AGCTCACGTTCTCTCGATGTGCTGAGAACAAACTTCACTCAAGCTGGCCATGT TGCTGGCTCTGGGCCACAGGGGCAATCAAAGATTTCCTCAAATCCCTGGCAC CTGGAGCTCGAGGTGTTCCCTCACTGTCATGGCCCTGGAGGCATCTACTCCC AGCTGGAGACCCCTGATTGAGCAGGAGCTCCAGGCATTAGAGGAGCTCTCTCAGC CTGCGGGCGACTCTGCTCTGCCCTGGCTGGCTCTGCTTCTGCCAACCTC AGCTACAATGCACTGACCGCCCTAGACAGCTCCCTGCCCTTGTGAGCTCTGCGTT TCTGAACCTAAAGCACAACTCAAGTCCAGGACTGTGAGGATTCTGATGGATTGTG TGAGCTCACCACATGGACATCCTCTATAATCGCTGCAATTGGTGCACAAATGGGA CCCTCAGGGCTGCTCTGGGGCTCTGATACTGCGAGGCAATGAGCTTCGGAGCCTG CAGGCCATGAGCAGCTGAGGAATCTGCGCACCTGGATTGGCATACAACCTGCTGG AGGACACCGGGAGCTGACCAACTGCTGGCTGGCTGAGCTCCGCAAGCTACCTG GAGGGAAACCCCTTTGGTCTCACCTGAGCACCAGGAGCAGCCACTGCCAGTACTTGT CACCCCCGGGCCAGGGATGTCGACTCTGGCTCTCTGATGGCAAGGTCTGTACT GACAGATTTCAGCAGACTCACACATCCTGGGCTCAGCCCCATGGCCCACCTTG CCCTGGCAGTGGGAGTACTCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCC TCTCCTCAGGGGGTGTGACCCAGCCCTGCTCTATAAGTTAAGAGCCGAGTCCG TGTGAGGCGGGCAAGCATCTGTAACCCAGTGTACCGGACCCGGAGCCCCAACTCTG AACCCCTCTCCGGCTGGTGTCTGAGCAGCACCCGGAGCTGGAGCTATGAGCA GCTTCCGGAAACGTTCGGCCCAACTGCGTCAGTACAGGAGTCACCTGGAGCCTC CGGAAACCCCTCTCCGGCCACCCCCACTACTCTGACCCAGTGCACCTCCAGGCCAGC TCCCAGGGCCCCACACTGCACCCAGACCTTCACCCCGCAGGAGGAAGCCAGAGGCC CCCAGGAGTCACACAGAAAATGTCAGAGGGTCAGGGGGAGCACAGGAGGAGGA AGAGGAGAAGGGAGGAGGAGGAAGAGGAGCAGGACCAAGAGGAAGTGGAAAGCGGA GAGGAGGAGGAGGAGGAGGAAGAGGAGCAGGACCAAGAGGAAGTGGAAAGCGGA TCTGTCGCCCTTGTGGTGTGCCCCCTGGAGGGGCTGAGGGCTACGGGGAGGG ATGCTTCTCAGGGTCACTCTGCCCCACTGTGTTGAGGTGAACCTCAACGAGCTCG ACCTTGAGGAGCTGGAGCTCCAGACTGTCAGGAGCTGAGATAGAGCCGGAGGCC AGGGCCAGGGCTCCCCAGGCCACGGCTCTGAGATCTGCTCCCTGGAGCCCCATCT CAGTCTGCGCTTCTCTACATCTGCCCTGACCGCAGTGTGCTGCTGTTGACCCAGTCACCA ATGTGGCTGGGAACAGCTTGGGGAGGCCAGGACCTCTGCTGGTAGATTCAGTG TCTACGCTGTGGCATGAGTCAAGCCAGGAGGAGCAGGATGGGATTAGACAGTGAG GAAGGCTGGAGGGCTCTGTTCTAAAGACAGAATCTCTGTTGTTGCTCTAATGTC GTAGTGACCGACGTGGCTCTCTCGCTGTGCTGGGGAAACCCCAACAGGGAGCGGA ACAGGGAGAGCAGCTCTGGCTCTCTCGCTGTGCGAGCCCTGCTGCCACCTCT GGCCATGGTGACCACTTGACAGGGCCAAGAACAGGCCACCTCAGGCACCGAGCACCC GTGACCATGGTAGTGGAGGCTCAGTCCGCCCTGAGCGCTGTGGCTCCGCTCT GGACCAACGGACTCCGGCTCTCTGGAGTGTGAGGTCTCAGGATGCCAGGAGGAG TTCAGTGTGCTCAAGGTCCCACTGGCAGGCCACACTGGGGAGTTCATGT GCCCTGTGTTGTGCTGACCCAGGCTGTAACCTGTGAGGTGACTGGGGAGATGAG TGAGCTCCAGCTAGCTGGCTGAGCTGACCCCTGGCTGTTCCCTGAGGATCTGAGT GGCATAGAGCTGGGCTGGCAGGCCAGAGCCTGCGGCTAGAGTGGCAGCTGGGGCG GCCGCTGTGCTGCTGCCAGAGATGCCAGGCATTGCCGGCTTCTAGAGGAGCT CCTGGTGTCTGGCAGTCTGCCCCCTGCCCTGGAGGAACCTGTGAGTGGCAGCTGG GAGGAGGTCACCCCCCAGCACCCGCTCTGGCATTGGGAAACCTGAGACTCATCTGG | |

| | | | |
|---|--|---------|------------------|
| | GCTGTTTCCATCGGACTCCGGACAGTGATCCAAGAGGGCGCTGGCCCTTGACCGATGA GGTCCCACGCTGACCTGGCCCTGACCTCAGGAGCCACGCT | | |
| | ORF Start: ATG at 13 ORF Stop: TGA at 3304 | | |
| | SEQ ID NO: 356 | 1097 aa | MW at 121064.1kD |
| NOV127b, CG59971-02 Protein Sequence | MTTAQRDSLLWKLAGLLFESQDVLSGCSTLSSLPTLQQLNHVTELHLPWGPGQTGFVALPSHPADSPLVILQLQFLFDVLQKTLSLKLHVAGPGPTGPIKIFFFKSLRHLERGVPLHCLHGLRGISQLETLICRSRLQALEELLSACGGDFCSALPWLLSANFSYNA LTALDSSLRLLSARFLNLSHNQVQDCQGFLMDLCELHLDISYNRLHLPVRMGP5A ALGVLLLRGNELRSLPGLCQEQLRNRHLDLAYNLLEGHRELSPWLALLAEFLRKLYLEGNP LWFHPEHRAATAQYLSPRARDAAATGFLLDGKVLSLTDQQTHTSLGLSPMPGPPLPWPVGSTPETSGGPDLSDLSSGGVVTQPLLHKVSKSRVVRVRRASISEPSDTDPPEPRTLNPS AGFWVQQHPELELMSSFERFGRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGP DTAPRPSPPQEEARGPQESPQKMSEEVRAEPQEEEEEKEGKEEKEEGEMVEQGEEEA EEEEEEQDQKEVEAELCRPLLVCPLLEGPEGVRGRCFLRVTSIAHLFEVELQAARTLER LELQSLEAAEIPEAQAAQRSPRTGSDLLPGAPILSLRFSYICPDRQLRRLVLEPDA HAAVQELLAVLPTVNTVAREQLGEARDLLLGRFQCLRCGHFKPEEPRMGLDSEEWR PLFKTQESPAPCNCGSDHVVLLAVSRGTNPERKQGEQSLAPSPSASPVCBPPGHGD HLDRAKNSPQQAPSTRDHGSWSLSPAPERCGLRSVDHRLRLFLDVEVFSDAQEEFQCC LKVPVALAGHTGEFMCLVVVSDDRLYLLKVTGEMSEPPASWQLTLAVPLQDLSIEL GLAGOSLRLWEAGAGRCVLLPDRARHCRAFLEELLGVLQSLPPAWRNCSVATEEEVT PQHRLWPLLEKDSLEARQFFYLRAFLVEGEASVQLMLPSTCLVSLLLTPSTLFLDE DAAGSPAEPSPPAASGEASEKVVPPSGPGPAVVRVREQQPLSSVLLYRSAPEDLRL FYDEVSRLESFWALRVVCQEQLTALLAWIREPWEELFSIGLRTVIQEALALDR | | |

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 127B.

| Table 127B. Comparison of NOV127a against NOV127b. | | |
|---|---|--|
| Protein Sequence | NOV127a Residues/ Match Residues | Identities/ Similarities for the Matched Region |
| NOV127b | 1..1098 | 891/1098 (81%) |
| | 1..1097 | 891/1098 (81%) |

Further analysis of the NOV127a protein yielded the following properties shown in Table 127C.

| Table 127C. Protein Sequence Properties NOV127a | |
|--|---|
| PSort analysis: | 0.5163 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.2442 probability located in mitochondrial inner membrane; 0.2442 probability located in mitochondrial intermembrane space |
| SignalP analysis: | No Known Signal Sequence Predicted |

A search of the NOV127a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publications, yielded several

Table 127D. Geneseq Results for NOV127a

| Geneseq Identifier | Protein/Organism/Length [Patent #, Date] | NOV127a Residues/ Match Residues | Identities/ Similarities for the Matched Region | Expect Value |
|--------------------|---|----------------------------------|---|--------------|
| AAM39827 | Human polypeptide SEQ ID NO 2972 - Homo sapiens, 169 aa. [WO200153312-A1, 26-JUL-2001] | 375..528 14..167 | 140/154 (90%) 145/154 (93%) | 3e-78 |
| AAM41613 | Human polypeptide SEQ ID NO 6544 - Homo sapiens, 184 aa. [WO200153312-A1, 26-JUL-2001] | 375..528 29..182 | 140/154 (90%) 145/154 (93%) | 4e-78 |
| AAU19764 | Human novel extracellular matrix protein, Seq ID No 414 - Homo sapiens, 211 aa. [WO200155368-A1, 02-AUG-2001] | 444..647 13..209 | 157/207 (75%) 160/207 (76%) | 2e-75 |
| ABB19833 | Protein #1832 encoded by probe for measuring heart cell gene expression - Homo sapiens, 127 aa. [WO200157274-A2, 09-AUG-2001] | 409..535 1..127 | 127/127 (100%) 127/127 (100%) | 2e-70 |
| AAM67606 | Human bone marrow expressed probe encoded protein SEQ ID NO: 27912 - Homo sapiens, 127 aa. [WO200157276-A2, 09-AUG-2001] | 409..535 1..127 | 127/127 (100%) 127/127 (100%) | 2e-70 |

In a BLAST search of public sequence databases, the NOV127a protein was found to have homology to the proteins shown in the BLASTP data in Table 127E.

Table 127E. Public BLASTP Results for NOV127a

| Protein Accession Number | Protein/Organism/Length | NOV127a Residues/ Match Residues | Identities/ Similarities for the Matched Portion | Expect Value |
|--------------------------|--|----------------------------------|--|--------------|
| AAL49726 | LKB1-INTERACTING PROTEIN 1 - Homo sapiens (Human), 1099 aa. | 1..1098 12..1099 | 1077/1098 (98%) 1078/1098 (98%) | 0.0 |
| Q96PY9 | KIAA1898 PROTEIN - Homo sapiens (Human), 1013 aa (fragment). | 76..1098 1..1013 | 1003/1023 (98%) 1003/1023 (98%) | 0.0 |
| Q96CN3 | SIMILAR TO RIKEN CDNA | 288..1098 | 793/811 (97%) | 0.0 |

TRADEMARKS

| | | | | |
|--------|--|--|--|-------|
| Q9DBT7 | | | | (0.0) |
|--------|--|--|--|-------|

| | | | | |
|--------|--|-------------------|--------------------------------|-------|
| | musculus (Mouse), 1072 aa. | 1..1072 | 895/1098 (81%) | |
| Q9VMK9 | CG9044 PROTEIN - Drosophila melanogaster (Fruit fly), 1289 aa. | 12..433 8..463 | 139/459 (30%) 220/459 (47%) | 6e-38 |

PFam analysis predicts that the NOV127a protein contains the domains shown in the Table 127F.

Table 127F. Domain Analysis of NOV127a

| Pfam Domain | NOV127a Match Region | Identities/ Similarities for the Matched Region | Expect Value |
|---------------------------|----------------------|--|-----------------|
| LRR: domain 1 of 5 | 164..186 | 7/25 (28%) 15/25 (60%) | 2.5e+02 |
| LRR: domain 2 of 5 | 187..209 | 6/25 (24%) 16/25 (64%) | 2.5e+02 |
| LRR: domain 3 of 5 | 210..231 | 8/25 (32%) 13/25 (52%) | 83 |
| LRR: domain 4 of 5 | 233..254 | 9/25 (36%) 17/25 (68%) | 16 |
| LRR: domain 5 of 5 | 255..279 | 10/27 (37%) 19/27 (70%) | 22 |
| Pkinase_C: domain 1 of 1 | 620..629 | 5/11 (45%) 9/11 (82%) | 8.9 |
| rubredoxin: domain 1 of 2 | 669..686 | 5/18 (28%) 13/18 (72%) | 4.6 |
| rubredoxin: domain 2 of 2 | 708..713 | 5/6 (83%) 6/6 (100%) | 1.2e+03 |

Example B: Sequencing Methodology and Identification of NOVX Clones

- GeneCalling™ Technology:** This is a proprietary method of performing differential

database query [Nature Biotechnology 17: 198-203 (1999)]. cDNA was derived from various

human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then digested with up to as many as 120 pairs of restriction enzymes and pairs of linker-adaptors specific for each pair of restriction enzymes were ligated to the appropriate end. The restriction digestion generates a mixture of unique cDNA gene fragments. Limited PCR amplification is performed with primers homologous to the linker adapter sequence where one primer is biotinylated and the other is fluorescently labeled. The doubly labeled material is isolated and the fluorescently labeled single strand is resolved by capillary gel electrophoresis. A computer algorithm compares the electropherograms from an experimental and control group for each of the restriction digestions. This and additional sequence-derived information is used to predict the identity of each differentially expressed gene fragment using a variety of genetic databases. The identity of the gene fragment is confirmed by additional, gene-specific competitive PCR or by isolation and sequencing of the gene fragment.

2. **SeqCallingTM Technology:** cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

The NOVX nucleic acid sequences are derived by laboratory screening of cDNA library by the two-hybrid approach. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, are sequenced. In silico prediction was based on sequences available in CuraGen Corporation's proprietary sequence databases or in the public human sequence databases, and provided either the full length DNA sequence, or some portion thereof.

The laboratory screening was performed using the methods summarized below:

cDNA libraries were derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then directionally cloned into the appropriate two-hybrid vector (Gal4-activation domain (Gal4-AD) fusion). Such cDNA libraries as well as commercially available cDNA libraries from Clontech (Palo Alto, CA) were then transferred from E.coli into a CuraGen Corporation proprietary yeast strain (disclosed in U. S. Patents 6,057,101 and 6,083,693, incorporated herein by reference in their entireties).

Gal4-binding domain (Gal4-BD) fusions of a CuraGen Corporation proprietary library of human sequences was used to screen multiple Gal4-AD fusion cDNA libraries resulting in the selection of yeast hybrid diploids in each of which the Gal4-AD fusion contains an individual cDNA. Each sample was amplified using the polymerase chain reaction (PCR) using non-specific primers at the cDNA insert boundaries. Such PCR product was sequenced; sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions.

Physical clone: the cDNA fragment derived by the screening procedure, covering the entire open reading frame is, as a recombinant DNA, cloned into pACT2 plasmid (Clontech) used to make the cDNA library. The recombinant plasmid is inserted into the host and selected by the yeast hybrid diploid generated during the screening procedure by the mating of both CuraGen Corporation proprietary yeast strains N106' and YULH (U. S. Patents 6,057,101 and 6,083,693).

4. RACE: Techniques based on the polymerase chain reaction such as rapid amplification of cDNA ends (RACE), were used to isolate or complete the predicted sequence of the cDNA of the invention. Usually multiple clones were sequenced from one or more human samples to derive the sequences for fragments. Various human tissue samples from different donors were used for the RACE reaction. The sequences derived from these procedures were included in the SeqCalling Assembly process described in preceding paragraphs.

5. Exon Linking: The NOVX target sequences identified in the present invention were subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. **Table B1** shows the sequences of the PCR primers used for obtaining different clones. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on *in silico* predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thyroid, trachea.

from Invitrogen. The resulting bacterial clone has an insert covering the entire open reading

frame cloned into the pCR2.1 vector. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported herein.

6. Physical Clone:

Exons were predicted by homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein.

The PCR product derived by exon linking, covering the entire open reading frame, was cloned into the pCR2.1 vector from Invitrogen to provide clones used for expression and screening purposes.

Example C: Quantitative expression analysis of clones in various cells and tissues

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR). RTQ PCR was performed on an Applied Biosystems ABI PRISM® 7700 or an ABI PRISM® 7900 HT Sequence Detection System. Various collections of samples are assembled on the plates, and referred to as Panel 1 (containing normal tissues and cancer cell lines), Panel 2 (containing samples derived from tissues from normal and cancer sources), Panel 3 (containing cancer cell lines), Panel 4 (containing cells and cell lines from normal tissues and cells related to inflammatory conditions), Panel 5D/5I (containing human tissues and cell lines with an emphasis on

normal and diseased brain and CNS tissue degeneration), panel 6 (containing samples from normal and Alzheimer's diseased brains).

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

First, the RNA samples were normalized to reference nucleic acids such as constitutively expressed genes (for example, β -actin and GAPDH). Normalized RNA (5 μ l) was converted to cDNA and analyzed by RTQ-PCR using One Step RT-PCR Master Mix Reagents (Applied Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions.

In other cases, non-normalized RNA samples were converted to single strand cDNA (sscDNA) using Superscript II (Invitrogen Corporation; Catalog No. 18064-147) and random hexamers according to the manufacturer's instructions. Reactions containing up to 10 μ g of total RNA were performed in a volume of 20 μ l and incubated for 60 minutes at 42°C. This reaction can be scaled up to 50 μ g of total RNA in a final volume of 100 μ l. sscDNA samples are then normalized to reference nucleic acids as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions.

Probes and primers were designed for each assay according to Applied Biosystems Primer Express Software package (version I for Apple Computer's Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58°-60°C, primer optimal T_m = 59°C, maximum primer difference = 2°C, probe does not have 5'G, probe T_m must be 10°C greater than primer T_m , amplicon size 75bp to 100bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe, respectively. Their final

PCR conditions: When working with RNA samples, normalized RNA from each tissue and each cell line was spotted in each well of either a 96 well or a 384-well PCR plate (Applied Biosystems). PCR cocktails included either a single gene specific probe and primers set, or two multiplexed probe and primers sets (a set specific for the target clone and another gene-specific set multiplexed with the target probe). PCR reactions were set up using TaqMan® One-Step RT-PCR Master Mix (Applied Biosystems, Catalog No. 4313803) following manufacturer's instructions. Reverse transcription was performed at 48°C for 30 minutes followed by amplification/PCR cycles as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying by 100.

When working with sscDNA samples, normalized sscDNA was used as described previously for RNA samples. PCR reactions containing one or two sets of probe and primers were set up as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions. PCR amplification was performed as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were analyzed and processed as described previously.

Panels 1, 1.1, 1.2, and 1.3D

The plates for Panels 1, 1.1, 1.2 and 1.3D include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in these panels are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in these panels are widely available through the American

comprised of samples derived from all major organ systems from single adult individuals or

fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose.

In the results for Panels 1, 1.1, 1.2 and 1.3D, the following abbreviations are used:

ca. = carcinoma,
* = established from metastasis,
met = metastasis,
s cell var = small cell variant,
non-s = non-sm = non-small,
squam = squamous,
pl. eff = pl effusion = pleural effusion,
glio = glioma,
astro = astrocytoma, and
neuro = neuroblastoma.

General_screening_panel_v1.4

The plates for Panel 1.4 include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in Panel 1.4 are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in Panel 1.4 are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on Panel 1.4 are comprised of pools of samples derived from all major organ systems from 2 to 5 different adult individuals or fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine.

Panels 2D and 2.2

The plates for Panels 2D and 2.2 generally include 2 control wells and 94 test samples composed of RNA or cDNA isolated from human tissue procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI). The tissues are derived from human malignancies and in cases where indicated many malignant tissues have "matched margins" obtained from noncancerous tissue just adjacent to the tumor. These are termed normal adjacent tissues and are denoted "NAT" in the results below. The tumor tissue and the "matched margins" are evaluated by two independent pathologists (the surgical pathologists and again by a pathologist at NDRI or CHTN). This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples include the original surgical pathology report that provides information regarding the clinical stage of the patient. These matched margins are taken from the tissue surrounding (i.e. immediately proximal) to the zone of surgery (designated "NAT", for normal adjacent tissue, in Table RR). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims (accidents, etc.). These tissues were ascertained to be free of disease and were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen.

Panel 3D

The plates of Panel 3D are comprised of 94 cDNA samples and two control samples. Specifically, 92 of these samples are derived from cultured human cancer cell lines, 2 samples of human primary cerebellar tissue and 2 controls. The human cell lines are generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: Squamous cell carcinoma of the tongue, breast cancer, prostate cancer, melanoma, epidermoid carcinoma, sarcomas, bladder carcinomas, pancreatic cancers, kidney cancers, leukemias/lymphomas, ovarian/uterine/cervical, gastric, colon, lung and CNS cancer cell lines. In addition, there are two independent samples of cerebellum. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. The cell lines in panel 3D and 1-3D are of the most common cell lines

Panels 4D, 4R, and 4.1D

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4R) or cDNA (Panels 4D/4.1D) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene, La Jolla, CA) and thymus and kidney (Clontech) was employed. Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as indicated. The following cytokines were used; IL-1 beta at approximately 1-5ng/ml, TNF alpha at approximately 5-10ng/ml, IFN gamma at approximately 20-50ng/ml, IL-4 at approximately 5-10ng/ml, IL-9 at approximately 5-10ng/ml, IL-13 at approximately 5-10ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100μM non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20ng/ml PMA and 1-2μg/ml ionomycin, IL-12 at 5-10ng/ml, IFN gamma at 20-50ng/ml and IL-18 at 5-10ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5μg/ml. Samples were

and mixing the isolated mononuclear cells in a final concentration of approximately 2×10^6 cells/ml in DMEM 5% FCS (Hyclone), 100μM non essential amino acids (Gibco), 1mM

sodium pyruvate (Gibco), mercaptoethanol (5.5×10^{-5} M) (Gibco), and 10mM Hepes (Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions.

Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum (FCS) (Hyclone, Logan, UT), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco), 50ng/ml GMCSF and 5ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10mM Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10 μ g/ml for 6 and 12-14 hours.

CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and positive selection. CD45RO beads were then used to isolate the CD45RO CD4 lymphocytes with the remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were placed in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) and plated at 10^6 cells/ml onto Falcon 6 well tissue culture plates that had been coated overnight with 0.5 μ g/ml anti-CD28 (Pharmingen) and 3ug/ml anti-CD3 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested the cells and expanded them in DMEM 5% FCS

cells were then activated again with plate bound anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and 24 hours after the second activation and after 4

days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10 $^{-5}$ M (Gibco), and 10mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and resuspended at 10 6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10 $^{-5}$ M (Gibco), and 10mM Hepes (Gibco). To activate the cells, we used PWM at 5 μ g/ml or anti-CD40 (Pharmingen) at approximately 10 μ g/ml and IL-4 at 5-10ng/ml. Cells were harvested for RNA preparation at 24,48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10 μ g/ml anti-CD28 (Pharmingen) and 2 μ g/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes (Poietic Systems, German Town, MD) were cultured at 10 5 -10 6 cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10 $^{-5}$ M (Gibco), 10mM Hepes (Gibco) and IL-2 (4ng/ml). IL-12 (5ng/ml) and anti-IL4 (1 μ g/ml) were used to direct to Th1, while IL-4 (5ng/ml) and anti-IFN gamma (1 μ g/ml) were used to direct to Th2 and IL-10 at 5ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for 4-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10 $^{-5}$ M (Gibco), 10mM Hepes (Gibco) and IL-2 (1ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1 μ g/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and third activation cycle.

KU-812. EOL cells were further differentiated by culture in 0.1mM dbcAMP at 5x10 5 cells/ml

for 8 days, changing the media every 3 days and adjusting the cell concentration to 5×10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), 10mM Hepes (Gibco). RNA was either prepared from resting cells or cells activated with PMA at 10ng/ml and ionomycin at 1 μ g/ml for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco). CCD1106 cells were activated for 6 and 14 hours with approximately 5 ng/ml TNF alpha and 1ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5ng/ml IL-4, 5ng/ml IL-9, 5ng/ml IL-13 and 25ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropene (Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at 14,000 rpm in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15ml Falcon Tube. An equal volume of isopropanol was added and left at -20°C overnight. The precipitated RNA was spun down at 9,000 rpm for 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was redissolved in 300 μ l of RNase-free water and 35 μ l buffer (Promega) 5 μ l DTT, 7 μ l RNAsin and 8 μ l DNase were added. The tube was incubated at 37°C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed in RNase free water. RNA was stored at -80°C.

AI_comprehensive panel_v1.0

The plates for AI_comprehensive panel_v1.0 include two control wells and 89 test samples comprised of cDNA isolated from surgical and postmortem human tissues obtained from the Backus Hospital and Clinomics (Frederick, MD). Total RNA was extracted from tissue samples from the Backus Hospital in the Facility at CuraGen. Total RNA from other

Joint tissues including synovial fluid, synovium, bone and cartilage were obtained from patients undergoing total knee or hip replacement surgery at the Backus Hospital. Tissue samples were immediately snap frozen in liquid nitrogen to ensure that isolated RNA was of optimal quality and not degraded. Additional samples of osteoarthritis and rheumatoid arthritis joint tissues were obtained from Clinomics. Normal control tissues were supplied by Clinomics and were obtained during autopsy of trauma victims.

Surgical specimens of psoriatic tissues and adjacent matched tissues were provided as total RNA by Clinomics. Two male and two female patients were selected between the ages of 25 and 47. None of the patients were taking prescription drugs at the time samples were isolated.

Surgical specimens of diseased colon from patients with ulcerative colitis and Crohn's disease and adjacent matched tissues were obtained from Clinomics. Bowel tissue from three female and three male Crohn's patients between the ages of 41-69 were used. Two patients were not on prescription medication while the others were taking dexamethasone, phenobarbital, or tylenol. Ulcerative colitis tissue was from three male and four female patients. Four of the patients were taking lebvid and two were on phenobarbital.

Total RNA from post mortem lung tissue from trauma victims with no disease or with emphysema, asthma or COPD was purchased from Clinomics. Emphysema patients ranged in age from 40-70 and all were smokers, this age range was chosen to focus on patients with cigarette-linked emphysema and to avoid those patients with alpha-1 anti-trypsin deficiencies. Asthma patients ranged in age from 36-75, and excluded smokers to prevent those patients that could also have COPD. COPD patients ranged in age from 35-80 and included both smokers and non-smokers. Most patients were taking corticosteroids, and bronchodilators.

In the labels employed to identify tissues in the AI_comprehensive panel_v1.0 panel, the following abbreviations are used:

AI = Autoimmunity
Syn = Synovial
Normal = No apparent disease

OAR = Osteoarthritis
(SS) (BA) (MF) = Individual patients

Adj = Adjacent tissue

Match control = adjacent tissues

-M = Male

-F = Female

COPD = Chronic obstructive pulmonary disease

Panels 5D and 5I

The plates for Panel 5D and 5I include two control wells and a variety of cDNAs isolated from human tissues and cell lines with an emphasis on metabolic diseases. Metabolic tissues were obtained from patients enrolled in the Gestational Diabetes study. Cells were obtained during different stages in the differentiation of adipocytes from human mesenchymal stem cells. Human pancreatic islets were also obtained.

In the Gestational Diabetes study subjects are young (18 - 40 years), otherwise healthy women with and without gestational diabetes undergoing routine (elective) Caesarean section. After delivery of the infant, when the surgical incisions were being repaired/closed, the obstetrician removed a small sample (<1 cc) of the exposed metabolic tissues during the closure of each surgical level. The biopsy material was rinsed in sterile saline, blotted and fast frozen within 5 minutes from the time of removal. The tissue was then flash frozen in liquid nitrogen and stored, individually, in sterile screw-top tubes and kept on dry ice for shipment to or to be picked up by CuraGen. The metabolic tissues of interest include uterine wall (smooth muscle), visceral adipose, skeletal muscle (rectus) and subcutaneous adipose. Patient descriptions are as follows:

| | |
|-------------|---|
| Patient 2 | Diabetic Hispanic, overweight, not on insulin |
| Patient 7-9 | Nondiabetic Caucasian and obese (BMI>30) |
| Patient 10 | Diabetic Hispanic, overweight, on insulin |
| Patient 11 | Nondiabetic African American and overweight |
| Patient 12 | Diabetic Hispanic on insulin |

Adipocyte differentiation was induced in donor progenitor cells obtained from Osiris (a division of Clonetics/BioWhittaker) in triplicate, except for Donor 3U which had only two replicates. Scientists at Clonetics isolated, grew and differentiated human mesenchymal stem cells (HuMSCs) for CuraGen based on the published protocol found in Mark F. Pittenger, et al. Multilineage Potential of Adult Human Mesenchymal Stem Cells Science Apr 2 1999.

Donor 2 and 3 U: Mesenchymal Stem cells, Undifferentiated Adipose
Donor 2 and 3 AM: Adipose, AdiposeMidway Differentiated
Donor 2 and 3 AD: Adipose, Adipose Differentiated

Human cell lines were generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: kidney proximal convoluted tubule, uterine smooth muscle cells, small intestine, liver HepG2 cancer cells, heart primary stromal cells, and adrenal cortical adenoma cells. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. All samples were processed at CuraGen to produce single stranded cDNA.

Panel 5I contains all samples previously described with the addition of pancreatic islets from a 58 year old female patient obtained from the Diabetes Research Institute at the University of Miami School of Medicine. Islet tissue was processed to total RNA at an outside source and delivered to CuraGen for addition to panel 5I.

In the labels employed to identify tissues in the 5D and 5I panels, the following abbreviations are used:

GO Adipose = Greater Omentum Adipose
SK = Skeletal Muscle
UT = Uterus
PL = Placenta
AD = Adipose Differentiated
AM = Adipose Midway Differentiated
U = Undifferentiated Stem Cells

Panel CNSD.01

The plates for Panel CNSD.01 include two control wells and 94 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center. Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

disease, Progressive Subnuclear Palsy, Depression, and Normal controls. Within each of these brains, the following regions are represented: cingulate gyrus, temporal pole, globus

pallidus, substantia nigra, Brodmann Area 4 (primary motor strip), Brodmann Area 7 (parietal cortex), Brodmann Area 9 (prefrontal cortex), and Brodmann area 17 (occipital cortex). Not all brain regions are represented in all cases; e.g., Huntington's disease is characterized in part by neurodegeneration in the globus pallidus, thus this region is impossible to obtain from confirmed Huntington's cases. Likewise Parkinson's disease is characterized by degeneration of the substantia nigra making this region more difficult to obtain. Normal control brains were examined for neuropathology and found to be free of any pathology consistent with neurodegeneration.

In the labels employed to identify tissues in the CNS panel, the following abbreviations are used:

PSP = Progressive supranuclear palsy

Sub Nigra = Substantia nigra

Glob Palladus= Globus pallidus

Temp Pole = Temporal pole

Cing Gyr = Cingulate gyrus

BA 4 = Brodmann Area 4

Panel CNS_Neurodegeneration_V1.0

The plates for Panel CNS_Neurodegeneration_V1.0 include two control wells and 47 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center (McLean Hospital) and the Human Brain and Spinal Fluid Resource Center (VA Greater Los Angeles Healthcare System). Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains six brains from Alzheimer's disease (AD) patients, and eight brains from "Normal controls" who showed no evidence of dementia prior to death. The eight normal control brains are divided into two categories: Controls with no dementia and no Alzheimer's like pathology (Controls) and controls with no dementia but evidence of severe Alzheimer's like pathology, (specifically

hippocampus, temporal cortex (Brodmann area 21), parietal cortex (Brodmann area 40), and occipital cortex (Brodmann area 17). These regions were chosen to encompass all levels of

neurodegeneration in AD. The hippocampus is a region of early and severe neuronal loss in AD; the temporal cortex is known to show neurodegeneration in AD after the hippocampus; the parietal cortex shows moderate neuronal death in the late stages of the disease; the occipital cortex is spared in AD and therefore acts as a "control" region within AD patients. Not all brain regions are represented in all cases.

In the labels employed to identify tissues in the CNS_Neurodegeneration_V1.0 panel, the following abbreviations are used:

AD = Alzheimer's disease brain; patient was demented and showed AD-like pathology upon autopsy

Control = Control brains; patient not demented, showing no neuropathology

Control (Path) = Control brains; patient not demented but showing sever AD-like pathology

SupTemporal Ctx = Superior Temporal Cortex

Inf Temporal Ctx = Inferior Temporal Cortex

A. CG58522-01: HUMAN PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA

Expression of gene CG58522-01 was assessed using the primer-probe set Ag3365, described in Table AA. Results of the RTQ-PCR runs are shown in Table AB.

Table AA. Probe Name Ag3365

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -cagaatgaaccaaggagactca -3' | 22 | 3 | 357 |
| Probe | TET-5' -ctactccgcatgcggcagaagacatt -3' - TAMRA | 26 | 35 | 358 |
| Reverse | 5' -cacatccatctgtcatctcctt -3' | 22 | 62 | 359 |

Table AB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3365, Run 216709759 | Tissue Name | Rel. Exp.(%) Ag3365, Run 216709759 |
|-------------------------|---------------------------------------|-----------------|---------------------------------------|
| Adipose | 0.0 | Renal ca. TK-10 | 0.0 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 0.0 |

| | | | |
|---------------|---|---------------------|---|
| Melanoma* M-4 | [| Gastric ca. NCI-H18 |] |
| Melanoma* | [| Colon ca. SW-948 |] |

| | | | |
|-------------------------------|------|----------------------------------|------|
| LOXIMVI | | | |
| Melanoma* SK-MEL-5 | 0.0 | Colon ca. SW480 | 0.0 |
| Squamous cell carcinoma SCC-4 | 0.0 | Colon ca.* (SW480 met) SW620 | 0.0 |
| Testis Pool | 10.7 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 0.0 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 0.0 |
| Placenta | 0.0 | Colon cancer tissue | 0.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.0 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 4.9 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.0 | Colon Pool | 0.0 |
| Ovarian ca. OVCAR-5 | 0.0 | Small Intestine Pool | 0.0 |
| Ovarian ca. IGROV-1 | 7.9 | Stomach Pool | 0.0 |
| Ovarian ca. OVCAR-8 | 26.8 | Bone Marrow Pool | 0.0 |
| Ovary | 0.0 | Fetal Heart | 0.0 |
| Breast ca. MCF-7 | 0.0 | Heart Pool | 0.0 |
| Breast ca. MDA-MB-231 | 1.7 | Lymph Node Pool | 16.5 |
| Breast ca. BT 549 | 0.0 | Fetal Skeletal Muscle | 0.0 |
| Breast ca. T47D | 0.0 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 0.0 |
| Breast Pool | 0.0 | Thymus Pool | 0.0 |
| Trachea | 0.0 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.0 |
| Fetal Lung | 0.0 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 3.3 | CNS cancer (astro) | 0.0 |
| Lung ca. SHP-77 | 0.0 | CNS cancer (glio) SI-295 | 25.7 |

| | | | |
|-------------------|-------|-------------------------------|-----|
| Lung ca. A549 | 0.0 | Brain (Amygdala) Pool | 0.0 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 0.0 |
| Lung ca. NCI-H23 | 100.0 | Brain (fetal) | 0.0 |
| Lung ca. NCI-H460 | 0.0 | Brain (Hippocampus) Pool | 4.8 |
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 0.0 |
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) Pool | 1.8 |
| Liver | 0.0 | Brain (Thalamus) Pool | 3.6 |
| Fetal Liver | 0.0 | Brain (whole) | 6.9 |
| Liver ca. HepG2 | 0.0 | Spinal Cord Pool | 0.0 |
| Kidney Pool | 0.0 | Adrenal Gland | 0.0 |
| Fetal Kidney | 0.0 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 0.0 |
| Renal ca. A498 | 0.0 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 0.0 |
| Renal ca. UO-31 | 0.0 | Pancreas Pool | 0.0 |

CNS_neurodegeneration_v1.0 Summary: Ag3365 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3365 - Significant expression of this gene is seen only in the lung cancer cell line NCI-H23 (CT=33.1). Therefore, expression of this gene may be used to distinguish this sample from the other samples on this panel.

Panel 4D Summary: Ag3365 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

B. CG58520-01: GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1

Expression of gene CG58520-01 was assessed using the primer-probe set Ag3364, described in Table BA.

Table BA. Probe Name Ag3364

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|-----------|--------|----------------|------------|
|---------|-----------|--------|----------------|------------|

| | | | | |
|---------|-------------------------|----|-----|-----|
| Reverse | ttcatctatggatccatcgatcc | 22 | 196 | 362 |
|---------|-------------------------|----|-----|-----|

CNS_neurodegeneration_v1.0 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel CNS_1 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

C. CG58520-03: GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR)

Expression of gene CG58520-03 was assessed using the primer-probe set Ag5092, described in Table CA.

Table CA. Probe Name Ag5092

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-gaacattcctgtccactgga-3' | 20 | 625 | 363 |
| Probe | TET-5'-atttcaagcgatggataccctaaaa-3' - TAMRA | 26 | 645 | 364 |
| Reverse | 5'-cacttctacggagggcttt-3' | 20 | 692 | 365 |

CNS_neurodegeneration_v1.0 Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.5 Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

D. CG58518-01: GAMMA-AMINOBUTYRIC ACID RECEPTOR RHO-3

Expression of gene CG58518-01 was assessed using the primer-probe sets Ag3363, Ag1130, Ag1198, Ag1253 and Ag1603, described in Tables DA, DB, DC, DD and DE. Results of the RTQ-PCR runs are shown in Tables DF, DG and DH.

Table DA. Probe Name Ag3363

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -tggcttcagtttagtctcctt-3' | 22 | 14 | 366 |
| Probe | TET-5' -cacctacatctggatcatattgaaacca-3' - TAMRA | 28 | 36 | 367 |
| Reverse | 5' -ttgatgttagaaggcagcacaaa-3' | 22 | 68 | 368 |

Table DB. Probe Name Ag1130

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -gtcctggcttcagtttagtct-3' | 22 | 10 | 369 |
| Probe | TET-5' -tcacacctacatctggatcatattgaaacca-3' - TAMRA | 29 | 35 | 370 |
| Reverse | 5' -ttgatgttagaaggcagcacaaa-3' | 22 | 68 | 371 |

Table DC. Probe Name Ag1198

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -gtcctggcttcagtttagtct-3' | 22 | 10 | 372 |
| Probe | TET-5' -tcacacctacatctggatcatattgaaacca-3' - TAMRA | 29 | 35 | 373 |
| Reverse | 5' -ttgatgttagaaggcagcacaaa-3' | 22 | 68 | 374 |

Table DD. Probe Name Ag1253

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -atctggtgccatatatcttt-3' | 22 | 466 | 375 |
| Probe | TET-5' -tgtccactctaaaagatccttcattcatga-3' - TAMRA | 30 | 489 | 376 |
| Reverse | 5' -cgcaaggatattctccatag-3' | 22 | 524 | 377 |

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|-----------|--------|----------------|------------|
| | | | | |

| | | | | |
|---------|--|----|----|-----|
| Forward | 5'-gtcctggcttccagtttagtct-3' | 22 | 10 | 378 |
| Probe | TET-5'-tcacctacatctggatcatattgaaacca-3' - TAMRA | 29 | 35 | 379 |
| Reverse | 5'-ttgatgttagaaggcagcacaaa-3' | 22 | 68 | 380 |

Table DF. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3363, Run 216709559 | Tissue Name | Rel. Exp.(%) Ag3363, Run 216709559 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 0.0 | Renal ca. TK-10 | 0.0 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 6.6 |
| Melanoma* Hs688(B).T | 0.0 | Gastric ca. (liver met.) NCI-N87 | 0.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 0.0 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |
| Melanoma* SK-MEL-5 | 0.0 | Colon ca. SW480 | 0.0 |
| Squamous cell carcinoma SCC-4 | 0.0 | Colon ca.* (SW480 met) SW620 | 0.0 |
| Testis Pool | 16.7 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 0.0 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 0.0 |
| Placenta | 0.0 | Colon cancer tissue | 0.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.0 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.0 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.0 | Colon Pool | 0.0 |
| Ovarian ca. OVCAR-5 | 0.0 | Small Intestine Pool | 0.0 |
| Ovarian ca. IGROV-1 | 0.0 | Stomach Pool | 0.0 |
| Ovarian ca. OVCAR-8 | 0.0 | Bone Marrow Pool | 0.0 |
| Ovary | 0.0 | Fetal Heart | 0.0 |
| Breast ca. MCF-7 | 0.0 | Heart Pool | 0.0 |

Breast ca. B1-24%

Fetal Skeletal Muscle

| | | | |
|-------------------|-------|-------------------------------------|------|
| Breast ca. T47D | 6.4 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 8.5 |
| Breast Pool | 0.0 | Thymus Pool | 0.0 |
| Trachea | 0.0 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 10.9 |
| Fetal Lung | 0.0 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 0.0 | CNS cancer (astro) SNB-75 | 0.0 |
| Lung ca. NCI-H146 | 77.9 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 100.0 | CNS cancer (glio) SF-295 | 11.4 |
| Lung ca. A549 | 10.1 | Brain (Amygdala) Pool | 0.0 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 0.0 |
| Lung ca. NCI-H23 | 34.4 | Brain (fetal) | 0.0 |
| Lung ca. NCI-H460 | 30.6 | Brain (Hippocampus) Pool | 0.0 |
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 0.0 |
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) Pool | 0.0 |
| Liver | 0.0 | Brain (Thalamus) Pool | 5.1 |
| Fetal Liver | 0.0 | Brain (whole) | 50.0 |
| Liver ca. HepG2 | 0.0 | Spinal Cord Pool | 0.0 |
| Kidney Pool | 3.0 | Adrenal Gland | 0.0 |
| Fetal Kidney | 8.4 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 0.0 |
| Renal ca. A498 | 0.0 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 0.0 |
| Renal ca. UO-31 | 0.0 | Pancreas Pool | 0.0 |

Table DG, Panel 1.2

| Tissue | Rel. Exp.(%) Ag1130, | Rel. Exp.(%) Ag1130, | Rel. Exp.(%) Ag1198, | Tissue | Rel. Exp.(%) Ag1130, | Rel. Exp.(%) Ag1130, | Rel. Exp.(%) Ag1130, |
|-------------|----------------------------|----------------------------|----------------------------|-------------|----------------------------|----------------------------|----------------------------|
| ENDOTHELIUM | 100.0 | 100.0 | 100.0 | ENDOTHELIUM | 100.0 | 100.0 | 100.0 |
| cells | 1 | 1 | 1 | 786-0 | 1 | 1 | 1 |

| | | | | | | | |
|------------------------------|-----|------|-----|--|------|------|-----|
| Heart (Fetal) | 0.0 | 0.0 | 0.0 | Renal ca. A498 | 7.3 | 4.7 | 0.0 |
| Pancreas | 0.0 | 0.0 | 0.0 | Renal ca. RXF 393 | 0.0 | 0.0 | 0.0 |
| Pancreatic ca. CAPAN 2 | 9.0 | 0.0 | 0.0 | Renal ca. ACHN | 0.0 | 0.0 | 0.0 |
| Adrenal Gland | 0.0 | 2.6 | 0.0 | Renal ca. UO-31 | 3.9 | 0.0 | 0.0 |
| Thyroid | 0.0 | 0.0 | 0.0 | Renal ca. TK-10 | 0.0 | 0.0 | 0.0 |
| Salivary gland | 0.0 | 0.0 | 0.0 | Liver | 26.6 | 0.0 | 0.0 |
| Pituitary gland | 0.0 | 0.0 | 0.0 | Liver (fetal) | 25.3 | 0.0 | 0.0 |
| Brain (fetal) | 0.0 | 0.0 | 0.0 | Liver ca. (hepatobla- st) HepG2 | 0.0 | 0.0 | 0.0 |
| Brain (whole) | 2.6 | 20.0 | 0.0 | Lung | 0.0 | 0.0 | 0.0 |
| Brain (amygdala) | 1.3 | 32.1 | 0.0 | Lung (fetal) | 0.0 | 0.0 | 0.0 |
| Brain (cerebellum) | 1.5 | 3.8 | 0.0 | Lung ca. (small cell) LX-1 | 3.4 | 0.0 | 0.0 |
| Brain (hippocamp- us) | 0.0 | 27.0 | 0.0 | Lung ca. (small cell) NCI- H69 | 28.5 | 74.2 | 0.0 |
| Brain (thalamus) | 9.9 | 22.5 | 9.8 | Lung ca. (s.cell var.) SHP-77 | 3.8 | 9.7 | 0.0 |
| Cerebral Cortex | 0.0 | 0.0 | 0.0 | Lung ca. (large cell) NCI- H460 | 8.8 | 4.1 | 5.3 |
| Spinal cord | 4.4 | 0.0 | 0.0 | Lung ca. (non-sm. cell) A549 | 51.4 | 9.5 | 7.2 |
| glio/astro cytoma MG | 0.0 | 0.0 | 0.0 | Lung ca. (non- small) A549 | 0.0 | 0.0 | 0.0 |

| do astro |
|----------|----------|----------|----------|----------|----------|----------|----------|
| U-118-MG | | | | U-118-MG | | | |

| | | | | HOP-62 | | | |
|---------------------|-----|------|-----|--------------------------------------|------|------|------|
| astrocytoma SW1783 | 2.9 | 0.0 | 0.0 | Lung ca. (non-s.cl) NCI-H522 | 0.0 | 0.0 | 0.0 |
| neuro*; met SK-N-AS | 0.0 | 0.0 | 0.0 | Lung ca. (squam.) SW 900 | 3.2 | 8.7 | 0.0 |
| astrocytoma SF-539 | 5.1 | 0.0 | 0.0 | Lung ca. (squam.) NCI-H596 | 2.3 | 15.9 | 0.0 |
| astrocytoma SNB-75 | 2.3 | 0.0 | 0.0 | Mammary gland | 0.0 | 0.0 | 0.0 |
| glioma SNB-19 | 6.3 | 20.7 | 9.0 | Breast ca.* (pl.ef) MCF-7 | 0.0 | 0.0 | 0.0 |
| glioma U251 | 1.4 | 0.0 | 1.8 | Breast ca.* (pl.ef) MDA-MB-231 | 0.0 | 0.0 | 0.0 |
| glioma SF-295 | 0.0 | 0.0 | 0.0 | Breast ca.* (pl. ef) T47D | 14.1 | 37.4 | 0.0 |
| Heart | 0.0 | 0.0 | 0.0 | Breast ca. BT-549 | 12.5 | 21.0 | 12.3 |
| Skeletal Muscle | 2.3 | 0.0 | 0.0 | Breast ca. MDA-N | 0.0 | 0.0 | 0.0 |
| Bone marrow | 0.0 | 0.0 | 0.0 | Ovary | 0.0 | 0.0 | 0.0 |
| Thymus | 0.0 | 0.0 | 0.0 | Ovarian ca. OVCAR-3 | 0.0 | 0.0 | 0.0 |
| Spleen | 2.2 | 0.0 | 0.0 | Ovarian ca. OVCAR-4 | 0.0 | 0.0 | 0.0 |
| Lymph node | 0.0 | 0.0 | 0.0 | Ovarian ca. OVCAR- | 66.9 | 35.4 | 4.4 |

| TISSUE | | | | OVCAK- | | | |
|--------|--|--|--|--------|--|--|--|
| | | | | | | | |

| | | | | | | | |
|----------------------------------|------|------|-------|-------------------------------|-------|-------|------|
| | | | | 8 | | | |
| Stomach | 0.0 | 0.0 | 0.0 | Ovarian ca. IGROV-1 | 6.0 | 0.0 | 0.0 |
| Small intestine | 5.4 | 0.0 | 0.0 | Ovarian ca. (ascites) SK-OV-3 | 30.8 | 0.0 | 0.0 |
| Colon ca. SW480 | 3.2 | 0.0 | 0.0 | Uterus | 0.0 | 0.0 | 0.0 |
| Colon ca.* SW620 (SW480 met) | 0.0 | 0.0 | 0.0 | Placenta | 0.0 | 0.0 | 0.0 |
| Colon ca. HT29 | 1.9 | 14.4 | 0.0 | Prostate | 6.9 | 0.0 | 0.0 |
| Colon ca. HCT-116 | 0.0 | 0.0 | 0.0 | Prostate ca.* (bone met) PC-3 | 100.0 | 0.0 | 0.0 |
| Colon ca. CaCo-2 | 0.0 | 0.0 | 0.0 | Testis | 54.7 | 100.0 | 36.9 |
| Colon ca. Tissue (ODO3866) | 72.2 | 75.8 | 100.0 | Melanoma Hs688(A).T | 4.2 | 0.0 | 0.0 |
| Colon ca. HCC-2998 | 5.3 | 4.8 | 0.0 | Melanoma* (met) Hs688(B).T | 2.7 | 34.2 | 13.3 |
| Gastric ca.* (liver met) NCI-N87 | 50.3 | 0.0 | 0.0 | Melanoma UACC-62 | 0.0 | 0.0 | 0.0 |
| Bladder | 6.0 | 22.1 | 0.0 | Melanoma M14 | 31.4 | 36.3 | 20.2 |
| Trachea | 0.0 | 0.0 | 0.0 | Melanoma LOX IMVI | 0.0 | 0.0 | 0.0 |
| Kidney | 2.0 | 0.0 | 0.0 | Melanoma* (met) SK-MEL-5 | 2.4 | 0.0 | 0.0 |
| Kidney | 1.1 | 2.5 | 0.0 | | | | |

| Tissue Name | Rel. Exp.(%) | Tissue Name | Rel. Exp.(%) |
|-------------|--------------|-------------|--------------|
|-------------|--------------|-------------|--------------|

| | Ag1198, Run 142014937 | | Ag1198, Run 142014937 |
|--------------------------------|----------------------------------|---|----------------------------------|
| Secondary Th1 act | 0.0 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 0.0 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 2.5 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 0.0 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvasular Dermal EC none | 0.0 |
| Primary Tr1 act | 0.0 | Microsvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 0.0 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 0.0 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 0.0 | Coronery artery SMC rest | 0.0 |
| CD45RO CD4 lymphocyte act | 0.0 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 0.0 |
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 0.0 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.0 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 0.0 |
| LAK cells rest | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 16.4 |
| LAK cells IL-2+IL-12 | 0.0 | Lupus kidney | 0.0 |
| LAK cells IL-2+IFN gamma | 0.0 | NCI-H292 none | 0.0 |

| | | | |
|--------------------|-----|----------------|-----|
| iMMA ionomycin | | | |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 0.0 |

| | | | |
|------------------------------|-----|---------------------------------------|-------|
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 0.0 |
| Two Way MLR 5 day | 0.0 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 0.0 |
| PBMC PWM | 0.0 | Lung fibroblast TNF alpha + IL-1 beta | 0.0 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 0.0 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 0.0 |
| B lymphocytes PWM | 0.0 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 rest | 0.0 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 0.0 | Dermal fibroblast IL-4 | 0.0 |
| Dendritic cells anti-CD40 | 0.0 | IBD Colitis 1 | 100.0 |
| Monocytes rest | 0.0 | IBD Colitis 2 | 0.0 |
| Monocytes LPS | 0.0 | IBD Crohn's | 0.0 |
| Macrophages rest | 0.0 | Colon | 0.0 |
| Macrophages LPS | 0.0 | Lung | 0.0 |
| HUVEC none | 0.0 | Thymus | 0.0 |
| HUVEC starved | 0.0 | Kidney | 0.0 |

CNS_neurodegeneration_v1.0 Summary: Ag3363 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3363 - Significant expression is seen in lung cancer cell line NCI-H146 (CT=34.5) and lung cancer cell line SHP-77 (CT=34.2). Therefore, expression of this can be used to distinguish these samples from the rest of the samples on this panel.

Ag3363 is expressed in significant amounts in two different lung cancer cell lines. It is also expressed in one lung cancer sample. Therefore, expression of this gene can be used to differentiate these samples.

from other samples on these panels. Results from a third experiment using the probe and primer set Ag1253 show low/undetectable levels of expression in all the samples on this panel.

Panel 1.3D Summary: Ag1253 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 2D Summary: Ag1603 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag1130/Ag1198/Ag1253/Ag3363 - Two experiments showed possible experimental difficulties, while the other three runs showed expression of this gene as low/undetectable (CTs > 35) across all of the samples on the panel.

Panel 4R Summary: Ag1198 - Significant expression of this gene is seen only in the IBD colitis 1 sample (CT=34.2). Therefore, expression of this gene can be used to differentiate this sample from others on the panel.

Panel CNS_1 Summary: Ag1253/Ag1603 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

E. CG58516-01: G-protein beta WD-40 repeats

Expression of gene CG58516-01 was assessed using the primer-probe set Ag3362, described in Table EA. Results of the RTQ-PCR runs are shown in Tables EB and EC.

Table EA. Probe Name Ag3362

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-gtcgcccaggaccttact-3' | 19 | 1474 | 381 |
| Probe | TET-5'-tcctacagctaattctgcaggcaca-3' - TAMRA | 26 | 1498 | 382 |
| Reverse | 5'-tacgcttactccgttaagtca-3' | 22 | 1543 | 383 |

Table EB. CNS_neurodegeneration_v1.0

| Sample | Control Pathway | Temporal Ctx |
|-------------|-----------------|--------------|
| Alain Hippo | | |

| | | | |
|----------------------------------|-------|-----------------------------------|------|
| AD 2 Hippo | 33.2 | Control (Path) 4 Temporal Ctx | 24.3 |
| AD 3 Hippo | 4.3 | AD 1 Occipital Ctx | 2.0 |
| AD 4 Hippo | 16.5 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 hippo | 96.6 | AD 3 Occipital Ctx | 5.4 |
| AD 6 Hippo | 43.2 | AD 4 Occipital Ctx | 24.7 |
| Control 2 Hippo | 29.1 | AD 5 Occipital Ctx | 24.5 |
| Control 4 Hippo | 16.6 | AD 6 Occipital Ctx | 31.9 |
| Control (Path) 3 Hippo | 3.8 | Control 1 Occipital Ctx | 0.9 |
| AD 1 Temporal Ctx | 7.1 | Control 2 Occipital Ctx | 89.5 |
| AD 2 Temporal Ctx | 23.2 | Control 3 Occipital Ctx | 12.6 |
| AD 3 Temporal Ctx | 5.6 | Control 4 Occipital Ctx | 6.3 |
| AD 4 Temporal Ctx | 20.0 | Control (Path) 1 Occipital Ctx | 65.1 |
| AD 5 Inf Temporal Ctx | 100.0 | Control (Path) 2 Occipital Ctx | 15.8 |
| AD 5 Sup Temporal Ctx | 43.8 | Control (Path) 3 Occipital Ctx | 2.0 |
| AD 6 Inf Temporal Ctx | 30.8 | Control (Path) 4 Occipital Ctx | 11.6 |
| AD 6 Sup Temporal Ctx | 69.7 | Control 1 Parietal Ctx | 2.8 |
| Control 1 Temporal Ctx | 9.0 | Control 2 Parietal Ctx | 39.2 |
| Control 2 Temporal Ctx | 59.0 | Control 3 Parietal Ctx | 23.5 |
| Control 3 Temporal Ctx | 11.7 | Control (Path) 1 Parietal Ctx | 69.7 |
| Control 4 Temporal Ctx | 8.2 | Control (Path) 2 Parietal Ctx | 14.9 |
| Control (Path) 1 Temporal Ctx | 56.3 | Control (Path) 3 Parietal Ctx | 0.9 |
| Control (Path) 2 Temporal Ctx | 34.2 | Control (Path) 4 Parietal Ctx | 38.7 |

Table EC. General screening panel v1.4

| ISSUE Name | Run 216523482 | ISSUE Name | Run 216523482 |
|------------|---------------|-----------------|---------------|
| Adipose | 6.3 | Renal ca. TK-10 | 44.1 |

| | | | |
|----------------------------------|-------|-------------------------------------|------|
| Melanoma* Hs688(A).T | 17.6 | Bladder | 9.4 |
| Melanoma* Hs688(B).T | 18.3 | Gastric ca. (liver met.) NCI-N87 | 21.6 |
| Melanoma* M14 | 17.1 | Gastric ca. KATO III | 17.6 |
| Melanoma* LOXIMVI | 13.6 | Colon ca. SW-948 | 5.8 |
| Melanoma* SK- MEL-5 | 19.6 | Colon ca. SW480 | 34.6 |
| Squamous cell carcinoma SCC-4 | 14.6 | Colon ca.* (SW480 met) SW620 | 14.2 |
| Testis Pool | 4.0 | Colon ca. HT29 | 7.2 |
| Prostate ca.* (bone met) PC-3 | 90.8 | Colon ca. HCT-116 | 14.3 |
| Prostate Pool | 4.0 | Colon ca. CaCo-2 | 19.8 |
| Placenta | 11.4 | Colon cancer tissue | 3.6 |
| Uterus Pool | 2.1 | Colon ca. SW1116 | 9.4 |
| Ovarian ca. OVCAR-3 | 17.4 | Colon ca. Colo-205 | 8.8 |
| Ovarian ca. SK-OV- 3 | 47.0 | Colon ca. SW-48 | 13.2 |
| Ovarian ca. OVCAR-4 | 14.7 | Colon Pool | 5.7 |
| Ovarian ca. OVCAR-5 | 31.6 | Small Intestine Pool | 10.2 |
| Ovarian ca. IGROV- 1 | 12.9 | Stomach Pool | 6.2 |
| Ovarian ca. OVCAR-8 | 6.7 | Bone Marrow Pool | 1.3 |
| Ovary | 12.5 | Fetal Heart | 1.1 |
| Breast ca. MCF-7 | 75.8 | Heart Pool | 3.4 |
| Breast ca. MDA- MB-231 | 30.4 | Lymph Node Pool | 8.7 |
| Breast ca. BT 549 | 65.5 | Fetal Skeletal Muscle | 2.3 |
| Breast ca. T47D | 100.0 | Skeletal Muscle Pool | 9.4 |
| Breast ca. MDA-N | 33.4 | Spleen Pool | 4.6 |
| Breast Pool | 4.6 | Thymus Pool | 7.3 |
| Trachea | 7.7 | CNS cancer (glio/astro) U87-MG | 33.9 |
| Lung | 4.9 | CNS cancer (glio/astro) | 27.2 |
| Lung ca. NCI-N417 | 9.3 | CNS cancer (astro) SF 539 | 14.3 |

| | | | |
|-------------------|------|----------------------------------|------|
| Lung ca. LX-1 | 15.8 | CNS cancer (astro) SNB-75 | 60.7 |
| Lung ca. NCI-H146 | 4.9 | CNS cancer (glio) SNB-19 | 13.8 |
| Lung ca. SHP-77 | 16.5 | CNS cancer (glio) SF-295 | 28.5 |
| Lung ca. A549 | 27.2 | Brain (Amygdala) Pool | 5.3 |
| Lung ca. NCI-H526 | 4.1 | Brain (cerebellum) | 5.0 |
| Lung ca. NCI-H23 | 15.0 | Brain (fetal) | 16.4 |
| Lung ca. NCI-H460 | 9.5 | Brain (Hippocampus) Pool | 5.5 |
| Lung ca. HOP-62 | 7.6 | Cerebral Cortex Pool | 8.7 |
| Lung ca. NCI-H522 | 18.2 | Brain (Substantia nigra) Pool | 8.3 |
| Liver | 0.0 | Brain (Thalamus) Pool | 6.3 |
| Fetal Liver | 7.3 | Brain (whole) | 7.0 |
| Liver ca. HepG2 | 29.5 | Spinal Cord Pool | 5.6 |
| Kidney Pool | 17.7 | Adrenal Gland | 6.3 |
| Fetal Kidney | 4.6 | Pituitary gland Pool | 0.8 |
| Renal ca. 786-0 | 17.2 | Salivary Gland | 5.6 |
| Renal ca. A498 | 5.1 | Thyroid (female) | 9.7 |
| Renal ca. ACHN | 17.3 | Pancreatic ca. CAPAN2 | 11.7 |
| Renal ca. UO-31 | 11.1 | Pancreas Pool | 9.2 |

CNS_neurodegeneration_v1.0 Summary: Ag3362 Highest expression of the CG58516-01 gene is seen in the occipital cortex of a control patient and the temporal cortex of an Alzheimer's patient. While the CG58516-01 gene does not appear to be preferentially expressed in Alzheimer's disease, this panel confirms expression of the CG58516-01 gene at moderate/high levels in the brain in an additional set of individuals. Please see Panel 1.4 for discussion of potential utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3362 The CG58516-01 gene is widely expressed in this panel, with highest expression in the breast cancer cell line T47D (CT=29). Significant expression is also seen in cell lines derived from prostate, breast and ovarian cancers. In general, expression of the CG58516-01 gene appears to be greater in the cancer cell lines than in normal tissue. Thus, the expression of this gene could be used to distinguish

normal tissue from cancerous tissue in a diagnostic assay.

CG58516-01 is also expressed in all brain regions examined. This gene encodes a protein with a

putative zinc-finger motif. Since these proteins are known to interact with nucleic acids, this suggests that this gene product may play a potential role in transcription. Thus, therapeutic modulation of the CG58516-01 gene product may be used to regulate the transcription of disease-related proteins such as ataxin, huntingtin, or various apoptosis cascade proteins.

Among tissues with metabolic function, this gene is expressed at low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, skeletal muscle, heart, and fetal liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that deregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

References:

- Zhu W, Chan EK, Li J, Hemmerich P, Tan EM. (2001) Transcription activating property of autoantigen SG2NA and modulating effect of WD-40 repeats. *Exp Cell Res.* 269(2):312-21

Panel 4D Summary: Ag3362 Results from one experiment with the CG58516-01 gene are not included because the amp plot corresponding to the run indicates that there were problems with the experiment.

F. CG58473-01: PROTEIN KINASE

Expression of gene CG58473-01 was assessed using the primer-probe set Ag3357, described in Table FA. Results of the RTQ-PCR runs are shown in Tables FB and FC.

Table FA. Probe Name Ag3357

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-gtcaagggtggccctaaaattc-3' | 21 | 853 | 384 |
| Probe | TET-5'-ccaggacacctatctccaagctgctta-3' - TAMRA | 26 | 897 | 385 |
| Reverse | 5'-agccgttctgaggggttat-3' | 19 | 926 | 386 |

Table FB. General screening panel v1.4

| Tissue Name | Ref. Exp. ID: Ag3357 Run 216523477 | Tissue Name | Ref. Exp. ID: Ag3357 Run 216523477 |
|-------------|---------------------------------------|-------------|---------------------------------------|
|-------------|---------------------------------------|-------------|---------------------------------------|

| | | | |
|-------------------------------|-------|-------------------------------------|------|
| Adipose | 0.0 | Renal ca. TK-10 | 13.2 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 7.2 |
| Melanoma* Hs688(B).T | 1.1 | Gastric ca. (liver met.) NCI-N87 | 5.4 |
| Melanoma* M14 | 50.0 | Gastric ca. KATO III | 49.0 |
| Melanoma* LOXIMVI | 33.0 | Colon ca. SW-948 | 14.9 |
| Melanoma* SK-MEL-5 | 24.7 | Colon ca. SW480 | 95.9 |
| Squamous cell carcinoma SCC-4 | 11.6 | Colon ca.* (SW480 met) SW620 | 53.6 |
| Testis Pool | 8.2 | Colon ca. HT29 | 10.3 |
| Prostate ca.* (bone met) PC-3 | 3.2 | Colon ca. HCT-116 | 76.3 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 14.1 |
| Placenta | 2.4 | Colon cancer tissue | 6.3 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 18.6 |
| Ovarian ca. OVCAR-3 | 51.1 | Colon ca. Colo-205 | 24.3 |
| Ovarian ca. SK-OV-3 | 53.2 | Colon ca. SW-48 | 26.1 |
| Ovarian ca. OVCAR-4 | 10.4 | Colon Pool | 4.6 |
| Ovarian ca. OVCAR-5 | 12.3 | Small Intestine Pool | 1.7 |
| Ovarian ca. IGROV-1 | 10.1 | Stomach Pool | 1.2 |
| Ovarian ca. OVCAR-8 | 13.4 | Bone Marrow Pool | 1.0 |
| Ovary | 0.0 | Fetal Heart | 0.0 |
| Breast ca. MCF-7 | 20.3 | Heart Pool | 0.0 |
| Breast ca. MDA-MB-231 | 65.1 | Lymph Node Pool | 1.4 |
| Breast ca. BT 549 | 100.0 | Fetal Skeletal Muscle | 0.0 |
| Breast ca. T47D | 34.2 | Skeletal Muscle Pool | 1.6 |
| Breast ca. MDA-N | 36.3 | Spleen Pool | 3.4 |
| Breast Pool | 1.3 | Thymus Pool | 4.7 |
| Trachea | 0.0 | CNS cancer (glio/astro) U87-MG | 7.8 |

Total radioactivity

NS cancer

(neuro)met) SK-N-AS

| | | | |
|-------------------|------|-------------------------------|------|
| Lung ca. NCI-N417 | 17.9 | CNS cancer (astro) SF-539 | 22.4 |
| Lung ca. LX-1 | 28.5 | CNS cancer (astro) SNB-75 | 19.2 |
| Lung ca. NCI-H146 | 74.7 | CNS cancer (glio) SNB-19 | 14.6 |
| Lung ca. SHP-77 | 40.6 | CNS cancer (glio) SF-295 | 3.0 |
| Lung ca. A549 | 64.6 | Brain (Amygdala) Pool | 0.0 |
| Lung ca. NCI-H526 | 23.8 | Brain (cerebellum) | 0.0 |
| Lung ca. NCI-H23 | 63.7 | Brain (fetal) | 0.0 |
| Lung ca. NCI-H460 | 0.8 | Brain (Hippocampus) Pool | 0.0 |
| Lung ca. HOP-62 | 2.0 | Cerebral Cortex Pool | 0.0 |
| Lung ca. NCI-H522 | 34.4 | Brain (Substantia nigra) Pool | 2.6 |
| Liver | 0.0 | Brain (Thalamus) Pool | 9.3 |
| Fetal Liver | 0.0 | Brain (whole) | 2.5 |
| Liver ca. HepG2 | 11.4 | Spinal Cord Pool | 0.0 |
| Kidney Pool | 0.0 | Adrenal Gland | 0.0 |
| Fetal Kidney | 3.1 | Pituitary gland Pool | 1.4 |
| Renal ca. 786-0 | 20.0 | Salivary Gland | 0.0 |
| Renal ca. A498 | 3.6 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 18.9 | Pancreatic ca. CAPAN2 | 20.4 |
| Renal ca. UO-31 | 10.4 | Pancreas Pool | 1.3 |

Table FC. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3357, Run 165231196 | Tissue Name | Rel. Exp.(%) Ag3357, Run 165231196 |
|--------------------|--|-------------------------------|--|
| Secondary Th1 act | 9.0 | HUVEC IL-1beta | 9.5 |
| Secondary Th2 act | 43.2 | HUVEC IFN gamma | 6.3 |
| Secondary Tr1 act | 46.0 | HUVEC TNF alpha + IFN gamma | 7.3 |
| Secondary Th1 rest | 6.7 | HUVEC TNF alpha + IL4 | 25.3 |
| Secondary Th2 rest | 12.2 | HUVEC IL-11 | 13.1 |
| Secondary Tr1 rest | 1.9 | Lung Microvascular EC none | 3.3 |
| | | Lung Microvascular EC | |

Primary Th1 act

| | | | | | |
|-----------------|---|------|------|-------------------------|-----|
| Primary Tr1 act | T | 33.0 | HODC | Microvascular Dermal EC | 7.3 |
|-----------------|---|------|------|-------------------------|-----|

| | | | |
|----------------------------------|------|--|------|
| | | TNFalpha + IL-1beta | |
| Primary Th1 rest | 28.1 | Bronchial epithelium TNFalpha + IL1beta | 1.9 |
| Primary Th2 rest | 12.1 | Small airway epithelium none | 3.6 |
| Primary Tr1 rest | 29.7 | Small airway epithelium TNFalpha + IL-1beta | 36.3 |
| CD45RA CD4 lymphocyte act | 28.5 | Coronery artery SMC rest | 0.0 |
| CD45RO CD4 lymphocyte act | 39.8 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 18.6 | Astrocytes rest | 1.4 |
| Secondary CD8 lymphocyte rest | 26.8 | Astrocytes TNFalpha + IL-1beta | 1.2 |
| Secondary CD8 lymphocyte act | 19.2 | KU-812 (Basophil) rest | 18.2 |
| CD4 lymphocyte none | 10.6 | KU-812 (Basophil) PMA/ionomycin | 30.4 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 15.6 | CCD1106 (Keratinocytes) none | 18.3 |
| LAK cells rest | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 7.7 |
| LAK cells IL-2 | 42.6 | Liver cirrhosis | 25.7 |
| LAK cells IL-2+IL-12 | 24.0 | Lupus kidney | 0.0 |
| LAK cells IL-2+IFN gamma | 24.8 | NCI-H292 none | 7.8 |
| LAK cells IL-2+ IL-18 | 40.3 | NCI-H292 IL-4 | 26.4 |
| LAK cells PMA/ionomycin | 0.0 | NCI-H292 IL-9 | 29.7 |
| NK Cells IL-2 rest | 23.5 | NCI-H292 IL-13 | 20.7 |
| Two Way MLR 3 day | 13.7 | NCI-H292 IFN gamma | 27.9 |
| Two Way MLR 5 day | 13.2 | HPAEC none | 8.6 |
| Two Way MLR 7 day | 11.7 | HPAEC TNF alpha + IL-1 beta | 2.4 |
| PBMC rest | 0.0 | Lung fibroblast none | 5.5 |
| PBMC PWM | 52.1 | Lung fibroblast TNF alpha + IL-1 beta | 2.2 |
| PBMC PHA-L | 14.6 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 16.5 | Lung fibroblast IL-9 | 0.0 |
| Ramos (B cell) | 1.4 | Lung fibroblast IL-13 | 0.0 |
| B lymphocytes CD40L and IL-4 | | | |
| | 10.4 | Dermal fibroblast CCD1070 rest | 40.1 |

| | | | |
|-------------------------------|------|--|------|
| EOL-1 dbcAMP | 9.9 | Dermal fibroblast CCD1070 TNF alpha | 43.8 |
| EOL-1 dbcAMP PMA/ionomycin | 13.2 | Dermal fibroblast CCD1070 IL-1 beta | 23.5 |
| Dendritic cells none | 4.7 | Dermal fibroblast IFN gamma | 3.7 |
| Dendritic cells LPS | 1.1 | Dermal fibroblast IL-4 | 4.6 |
| Dendritic cells anti- CD40 | 0.0 | IBD Colitis 2 | 0.0 |
| Monocytes rest | 0.0 | IBD Crohn's | 0.0 |
| Monocytes LPS | 0.0 | Colon | 28.1 |
| Macrophages rest | 4.3 | Lung | 59.0 |
| Macrophages LPS | 0.0 | Thymus | 0.0 |
| HUVEC none | 28.3 | Kidney | 10.0 |
| HUVEC starved | 25.3 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3357 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3357 This gene is primarily expressed in cancer cell lines, with highest expression in a breast cancer cell line BT 549(CT=32.8). This gene is expressed in the following cell lines but not the corresponding healthy tissue: gastric, brain, colon, lung, breast, ovarian cancer and melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

Panel 4D Summary: Ag3357 Highest expression of the CG58473-01 gene is seen in pokeweed mitogen-activated purified peripheral blood B lymphocytes (CT=33.2). In addition, no expression of the transcript is seen in PBMC that contain normal B cells, but the transcript is induced when PBMC are treated with the B cell selective pokeweed mitogen. The transcript is not seen in the B cell lymphoma cell line Ramos regardless of stimulation. Thus, the putative protein encoded by this gene could potentially be used diagnostically to identify activated B cells. Therefore, therapeutics that antagonize the function of this gene product may be useful as therapeutic drugs to reduce or eliminate the symptoms in patients with

colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

G. CG58470-01: UDP-N-ACETYLHEXOSAMINE PYROPHOSPHORYLASE

Expression of gene CG58470-01 was assessed using the primer-probe set Ag5940, described in Table GA.

Table GA. Probe Name Ag5940

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-atattcctgaagctacaacagtttagct-3' | 26 | 422 | 387 |
| Probe | TET-5'-tggcaacaaatgcattattccatattacg-3' - TAMRA | 29 | 459 | 388 |
| Reverse | 5'-gagtgaactcgctggtcatg-3' | 20 | 489 | 389 |

General screening panel v1.5 Summary: Ag5940 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 5 Islet Summary: Ag5940 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

H. CG58593-01: UBIQUITIN-52

Expression of gene CG58593-01 was assessed using the primer-probe set Ag3421, described in Table HA.

Table HA. Probe Name Ag3421

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-atctgctgcaagtgttatgc-3' | 20 | 291 | 390 |
| Probe | TET-5'-cggtgcttatcaactgccacaagaaga-3' - TAMRA | 26 | 323 | 391 |
| Reverse | 5'-tgaccttcttcctgggtac-3' | 20 | 371 | 392 |

CNS_neurodegeneration_v1.0 Summary: Ag3421 - Expression of this gene is

General screening panel v1.4 Summary - low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3421 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

I. CG57871-01: TOUSLED-LIKE KINASE

Expression of gene CG57871-01 was assessed using the primer-probe set Ag3351, described in Table IA. Results of the RTQ-PCR runs are shown in Tables IB and IC.

Table IA. Probe Name Ag3351

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -gatcctcaactgcaacattttt-3' | 22 | 346 | 393 |
| Probe | TET-5' -aatcccttaccgcgacgagtagaaaca-3' - TAMRA | 26 | 372 | 394 |
| Reverse | 5' -gcactgccatctaaaccataga-3' | 22 | 403 | 395 |

Table IB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3351, Run 210141594 | Tissue Name | Rel. Exp.(%) Ag3351, Run 210141594 |
|---------------------------|---------------------------------------|----------------------------------|---------------------------------------|
| AD 1 Hippo | 10.4 | Control (Path) 3 Temporal Ctx | 3.0 |
| AD 2 Hippo | 33.4 | Control (Path) 4 Temporal Ctx | 65.1 |
| AD 3 Hippo | 5.5 | AD 1 Occipital Ctx | 20.2 |
| AD 4 Hippo | 8.4 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 hippo | 100.0 | AD 3 Occipital Ctx | 3.8 |
| AD 6 Hippo | 33.4 | AD 4 Occipital Ctx | 45.1 |
| Control 2 Hippo | 29.9 | AD 5 Occipital Ctx | 15.2 |
| Control 4 Hippo | 6.7 | AD 6 Occipital Ctx | 46.7 |
| Control (Path) 3 Hippo | 3.7 | Control 1 Occipital Ctx | 2.7 |
| AD 1 Temporal Ctx | 16.8 | Control 2 Occipital Ctx | 52.5 |
| AD 2 Temporal Ctx | 45.1 | Control 3 Occipital Ctx | 45.4 |
| AD 3 Temporal Ctx | 6.9 | Control 4 Occipital Ctx | 6.3 |

| | | | |
|------------|------|-----------------------------------|------|
| AD 5 Hippo | 92.0 | Control (Path) 2 Occipital Ctx | 34.4 |
|------------|------|-----------------------------------|------|

| | | | |
|-------------------------------|------|--------------------------------|------|
| AD 5 SupTemporal Ctx | 13.0 | Control (Path) 3 Occipital Ctx | 0.8 |
| AD 6 Inf Temporal Ctx | 48.6 | Control (Path) 4 Occipital Ctx | 40.6 |
| AD 6 Sup Temporal Ctx | 56.6 | Control 1 Parietal Ctx | 6.9 |
| Control 1 Temporal Ctx | 6.2 | Control 2 Parietal Ctx | 48.0 |
| Control 2 Temporal Ctx | 29.3 | Control 3 Parietal Ctx | 26.1 |
| Control 3 Temporal Ctx | 32.8 | Control (Path) 1 Parietal Ctx | 73.7 |
| Control 4 Temporal Ctx | 13.9 | Control (Path) 2 Parietal Ctx | 57.4 |
| Control (Path) 1 Temporal Ctx | 79.6 | Control (Path) 3 Parietal Ctx | 3.4 |
| Control (Path) 2 Temporal Ctx | 97.3 | Control (Path) 4 Parietal Ctx | 78.5 |

Table IC, Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3351, Run 165222896 | Tissue Name | Rel. Exp.(%) Ag3351, Run 165222896 |
|--------------------|--|--|--|
| Secondary Th1 act | 16.5 | HUVEC IL-1beta | 15.4 |
| Secondary Th2 act | 26.4 | HUVEC IFN gamma | 13.5 |
| Secondary Tr1 act | 23.3 | HUVEC TNF alpha + IFN gamma | 17.0 |
| Secondary Th1 rest | 6.0 | HUVEC TNF alpha + IL4 | 11.0 |
| Secondary Th2 rest | 10.7 | HUVEC IL-11 | 5.4 |
| Secondary Tr1 rest | 2.1 | Lung Microvascular EC none | 12.4 |
| Primary Th1 act | 19.2 | Lung Microvascular EC TNFalpha + IL-1beta | 9.6 |
| Primary Th2 act | 17.6 | Microvascular Dermal EC none | 14.7 |
| Primary Tr1 act | 36.1 | Microvasular Dermal EC TNFalpha + IL-1beta | 14.8 |
| Primary Th1 rest | 55.5 | Bronchial epithelium TNFalpha + IL1beta | 14.1 |
| | | Small airway epithelium | |

| | | | | |
|------------|------|----------------------|--------------------------|------|
| CD45RA CD4 | 13.0 | IFN alpha + IL-1beta | Coronery artery SMC rest | 15.6 |
|------------|------|----------------------|--------------------------|------|

| | | | |
|--------------------------------|-------|---|------|
| lymphocyte act | | | |
| CD45RO CD4 lymphocyte act | 21.0 | Coronery artery SMC TNFalpha + IL-1beta | 6.1 |
| CD8 lymphocyte act | 12.9 | Astrocytes rest | 11.5 |
| Secondary CD8 lymphocyte rest | 14.9 | Astrocytes TNFalpha + IL-1beta | 11.8 |
| Secondary CD8 lymphocyte act | 14.8 | KU-812 (Basophil) rest | 19.2 |
| CD4 lymphocyte none | 10.7 | KU-812 (Basophil) PMA/ionomycin | 54.0 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 12.7 | CCD1106 (Keratinocytes) none | 12.2 |
| LAK cells rest | 17.2 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 9.0 |
| LAK cells IL-2 | 22.4 | Liver cirrhosis | 7.4 |
| LAK cells IL-2+IL-12 | 20.4 | Lupus kidney | 3.4 |
| LAK cells IL-2+IFN gamma | 37.9 | NCI-H292 none | 47.6 |
| LAK cells IL-2+ IL-18 | 18.6 | NCI-H292 IL-4 | 42.3 |
| LAK cells PMA/ionomycin | 10.5 | NCI-H292 IL-9 | 30.4 |
| NK Cells IL-2 rest | 17.8 | NCI-H292 IL-13 | 15.7 |
| Two Way MLR 3 day | 33.2 | NCI-H292 IFN gamma | 25.5 |
| Two Way MLR 5 day | 10.6 | HPAEC none | 13.5 |
| Two Way MLR 7 day | 9.9 | HPAEC TNF alpha + IL-1 beta | 17.7 |
| PBMC rest | 12.8 | Lung fibroblast none | 11.5 |
| PBMC PWM | 63.3 | Lung fibroblast TNF alpha + IL-1 beta | 12.4 |
| PBMC PHA-L | 18.0 | Lung fibroblast IL-4 | 31.2 |
| Ramos (B cell) none | 14.0 | Lung fibroblast IL-9 | 22.2 |
| Ramos (B cell) ionomycin | 77.9 | Lung fibroblast IL-13 | 27.4 |
| B lymphocytes PWM | 100.0 | Lung fibroblast IFN gamma | 44.8 |
| B lymphocytes CD40L and IL-4 | 30.8 | Dermal fibroblast CCD1070 rest | 33.7 |
| EOL-1 dbcAMP | 11.3 | Dermal fibroblast CCD1070 TNF alpha | 50.0 |
| EOL-1 dbcAMP | 13.7 | Dermal fibroblast | 13.4 |
| Dendritic cells LPS | 19.8 | Dermal fibroblast IL-4 | 25.7 |

| | | | |
|---------------------------|------|---------------|------|
| Dendritic cells anti-CD40 | 14.2 | IBD Colitis 2 | 2.0 |
| Monocytes rest | 22.5 | IBD Crohn's | 3.2 |
| Monocytes LPS | 32.8 | Colon | 26.8 |
| Macrophages rest | 31.0 | Lung | 14.6 |
| Macrophages LPS | 30.8 | Thymus | 28.7 |
| HUVEC none | 18.3 | Kidney | 45.4 |
| HUVEC starved | 45.7 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3351 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. While no differential expression of this gene is detected between Alzheimer's diseased postmortem brains and those of non-demented controls, the widespread expression of this gene in the brain suggests that therapeutic modulation of the expression or function of this gene may be effective in the treatment of neurologic disorders such as Parkinson's disease, epilepsy, stroke and multiple sclerosis.

General_screening_panel_v1.4 Summary: Ag3351 - Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 4D Summary: Ag3351 The CG57871-01 gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

J. CG58590-01 and CG58590-02: PAI S Guanylate kinase

probe set Ag3381, described in Table 1A. Results of the RT-PCR runs are shown in Tables

JB, JC and JD. Please note that CG58590-02 represents a full-length physical clone of the CG58590-01 gene, validating the prediction of the gene sequence.

Table JA. Probe Name Ag3380

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -tttgatacggaatttgtaatt-3' | 22 | 1931 | 396 |
| Probe | TET-5'-ccgatcttataaaggctatcaggaa-3' TAMRA | 26 | 1953 | 397 |
| Reverse | 5' -cccaactgagggttcagtatcaag-3' | 22 | 2000 | 398 |

Table JB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3380, Run 210153753 | Tissue Name | Rel. Exp.(%) Ag3380, Run 210153753 |
|---------------------------|---------------------------------------|-----------------------------------|---------------------------------------|
| AD 1 Hippo | 12.9 | Control (Path) 3 Temporal Ctx | 4.7 |
| AD 2 Hippo | 27.7 | Control (Path) 4 Temporal Ctx | 24.3 |
| AD 3 Hippo | 4.8 | AD 1 Occipital Ctx | 15.6 |
| AD 4 Hippo | 7.7 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 hippo | 100.0 | AD 3 Occipital Ctx | 7.5 |
| AD 6 Hippo | 64.2 | AD 4 Occipital Ctx | 19.1 |
| Control 2 Hippo | 25.5 | AD 5 Occipital Ctx | 29.5 |
| Control 4 Hippo | 9.9 | AD 6 Occipital Ctx | 40.1 |
| Control (Path) 3 Hippo | 8.4 | Control 1 Occipital Ctx | 4.2 |
| AD 1 Temporal Ctx | 17.6 | Control 2 Occipital Ctx | 65.5 |
| AD 2 Temporal Ctx | 25.3 | Control 3 Occipital Ctx | 13.4 |
| AD 3 Temporal Ctx | 4.9 | Control 4 Occipital Ctx | 6.4 |
| AD 4 Temporal Ctx | 17.4 | Control (Path) 1 Occipital Ctx | 78.5 |
| AD 5 Inf Temporal Ctx | 81.8 | Control (Path) 2 Occipital Ctx | 9.4 |
| AD 5 Sup Temporal | .. | Control (Path) 3 | .. |

| | | Occipital Ctx | |
|-------------------|------|--------------------|-----|
| AD 6 Sup Temporal | 53.6 | Control 1 Parietal | 6.0 |

| | | | |
|-------------------------------|------|-------------------------------|------|
| Ctx | | Ctx | |
| Control 1 Temporal Ctx | 5.7 | Control 2 Parietal Ctx | 37.1 |
| Control 2 Temporal Ctx | 34.6 | Control 3 Parietal Ctx | 16.5 |
| Control 3 Temporal Ctx | 10.2 | Control (Path) 1 Parietal Ctx | 67.4 |
| Control 4 Temporal Ctx | 7.1 | Control (Path) 2 Parietal Ctx | 18.7 |
| Control (Path) 1 Temporal Ctx | 41.5 | Control (Path) 3 Parietal Ctx | 3.3 |
| Control (Path) 2 Temporal Ctx | 29.5 | Control (Path) 4 Parietal Ctx | 34.4 |

Table JC. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3380, Run 217043276 | Tissue Name | Rel. Exp.(%) Ag3380, Run 217043276 |
|-------------------------------|------------------------------------|----------------------------------|------------------------------------|
| Adipose | 9.0 | Renal ca. TK-10 | 25.5 |
| Melanoma* Hs688(A).T | 18.9 | Bladder | 15.9 |
| Melanoma* Hs688(B).T | 16.8 | Gastric ca. (liver met.) NCI-N87 | 52.5 |
| Melanoma* M14 | 14.9 | Gastric ca. KATO III | 34.6 |
| Melanoma* LOXIMVI | 21.6 | Colon ca. SW-948 | 4.9 |
| Melanoma* SK-MEL-5 | 27.0 | Colon ca. SW480 | 82.4 |
| Squamous cell carcinoma SCC-4 | 28.7 | Colon ca.* (SW480 met) SW620 | 20.6 |
| Testis Pool | 5.1 | Colon ca. HT29 | 9.2 |
| Prostate ca.* (bone met) PC-3 | 59.9 | Colon ca. HCT-116 | 20.6 |
| Prostate Pool | 8.6 | Colon ca. CaCo-2 | 22.8 |
| Placenta | 3.9 | Colon cancer tissue | 10.1 |
| Uterus Pool | 1.9 | Colon ca. SW1116 | 6.2 |
| Ovarian ca. OVCAR-3 | 32.5 | Colon ca. Colo-205 | 4.9 |
| Ovarian ca. SK-OV-3 | 57.4 | Colon ca. SW-48 | 4.2 |

| | | | |
|--------------------------|------|-----------------------------|-----|
| IV affil. ca. OVCAR-5 | 13.1 | Stomach ca. Stomach Pool | 7.4 |
| Ovarian ca. IGROV- | | | |

| | | | |
|------------------------|-------|-------------------------------------|------|
| 1 | | | |
| Ovarian ca. OVCAR-8 | 19.2 | Bone Marrow Pool | 4.2 |
| Ovary | 5.9 | Fetal Heart | 6.3 |
| Breast ca. MCF-7 | 35.1 | Heart Pool | 4.9 |
| Breast ca. MDA-MB-231 | 58.2 | Lymph Node Pool | 11.4 |
| Breast ca. BT 549 | 26.8 | Fetal Skeletal Muscle | 3.3 |
| Breast ca. T47D | 100.0 | Skeletal Muscle Pool | 8.1 |
| Breast ca. MDA-N | 8.7 | Spleen Pool | 5.6 |
| Breast Pool | 10.4 | Thymus Pool | 6.3 |
| Trachea | 5.5 | CNS cancer (glio/astro) U87-MG | 39.2 |
| Lung | 3.8 | CNS cancer (glio/astro) U-118-MG | 54.7 |
| Fetal Lung | 11.8 | CNS cancer (neuro;met) SK-N-AS | 19.6 |
| Lung ca. NCI-N417 | 3.2 | CNS cancer (astro) SF-539 | 12.2 |
| Lung ca. LX-1 | 20.7 | CNS cancer (astro) SNB-75 | 29.7 |
| Lung ca. NCI-H146 | 3.8 | CNS cancer (glio) SNB-19 | 13.4 |
| Lung ca. SHP-77 | 17.9 | CNS cancer (glio) SF-295 | 28.9 |
| Lung ca. A549 | 30.6 | Brain (Amygdala) Pool | 11.8 |
| Lung ca. NCI-H526 | 3.6 | Brain (cerebellum) | 6.0 |
| Lung ca. NCI-H23 | 29.3 | Brain (fetal) | 8.4 |
| Lung ca. NCI-H460 | 14.8 | Brain (Hippocampus) Pool | 14.5 |
| Lung ca. HOP-62 | 19.5 | Cerebral Cortex Pool | 16.2 |
| Lung ca. NCI-H522 | 28.7 | Brain (Substantia nigra) Pool | 16.0 |
| Liver | 0.4 | Brain (Thalamus) Pool | 22.7 |
| Fetal Liver | 11.9 | Brain (whole) | 5.9 |
| Liver ca. HepG2 | 12.9 | Spinal Cord Pool | 16.0 |
| Kidney Pool | 18.4 | Adrenal Gland | 5.1 |
| Fetal Kidney | 22.8 | Pituitary gland Pool | 3.8 |
| Renal ca. 786-0 | 28.5 | Salivary Gland | 2.1 |
| Renal ca. A498 | 5.0 | Thyroid (female) | 8.2 |

Table JD, Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3380, Run 165296532 | Tissue Name | Rel. Exp.(%) Ag3380, Run 165296532 |
|--------------------------------|--|---|--|
| Secondary Th1 act | 13.1 | HUVEC IL-1beta | 15.0 |
| Secondary Th2 act | 14.6 | HUVEC IFN gamma | 19.6 |
| Secondary Tr1 act | 15.2 | HUVEC TNF alpha + IFN gamma | 28.3 |
| Secondary Th1 rest | 4.6 | HUVEC TNF alpha + IL4 | 26.1 |
| Secondary Th2 rest | 4.7 | HUVEC IL-11 | 7.8 |
| Secondary Tr1 rest | 8.0 | Lung Microvascular EC none | 25.5 |
| Primary Th1 act | 14.9 | Lung Microvascular EC TNFalpha + IL-1beta | 19.5 |
| Primary Th2 act | 13.2 | Microvascular Dermal EC none | 37.9 |
| Primary Tr1 act | 20.7 | Microvasular Dermal EC TNFalpha + IL-1beta | 24.8 |
| Primary Th1 rest | 35.6 | Bronchial epithelium TNFalpha + IL1beta | 37.1 |
| Primary Th2 rest | 24.0 | Small airway epithelium none | 15.0 |
| Primary Tr1 rest | 16.2 | Small airway epithelium TNFalpha + IL-1beta | 100.0 |
| CD45RA CD4 lymphocyte act | 23.3 | Coronery artery SMC rest | 30.1 |
| CD45RO CD4 lymphocyte act | 18.2 | Coronery artery SMC TNFalpha + IL-1beta | 13.6 |
| CD8 lymphocyte act | 7.4 | Astrocytes rest | 22.5 |
| Secondary CD8 lymphocyte rest | 13.4 | Astrocytes TNFalpha + IL-1beta | 21.2 |
| Secondary CD8 lymphocyte act | 4.4 | KU-812 (Basophil) rest | 17.9 |
| CD4 lymphocyte none | 8.0 | KU-812 (Basophil) PMA/ionomycin | 68.3 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 10.7 | CCD1106 (Keratinocytes) none | 22.1 |
| LAK cells rest | 13.5 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 9.2 |
| LAK cells IL-2 | 12.9 | Liver cirrhosis | 3.1 |
| LAK cells IL-2+IL-12 | 13.2 | Lupus kidney | 2.9 |
| LAK cells IL-2+IFN | | | |

| | | | |
|---------------|-----|---------------|------|
| LAK cells | 9.5 | NCI-H292 IL-9 | 29.5 |
| PMA/ionomycin | | | |

| | | | |
|------------------------------|------|---------------------------------------|------|
| NK Cells IL-2 rest | 7.0 | NCI-H292 IL-13 | 36.6 |
| Two Way MLR 3 day | 15.2 | NCI-H292 IFN gamma | 42.6 |
| Two Way MLR 5 day | 7.0 | HPAEC none | 14.3 |
| Two Way MLR 7 day | 9.6 | HPAEC TNF alpha + IL-1 beta | 25.9 |
| PBMC rest | 6.4 | Lung fibroblast none | 12.5 |
| PBMC PWM | 60.7 | Lung fibroblast TNF alpha + IL-1 beta | 11.0 |
| PBMC PHA-L | 18.8 | Lung fibroblast IL-4 | 25.9 |
| Ramos (B cell) none | 31.9 | Lung fibroblast IL-9 | 20.6 |
| Ramos (B cell) ionomycin | 94.0 | Lung fibroblast IL-13 | 18.8 |
| B lymphocytes PWM | 42.9 | Lung fibroblast IFN gamma | 23.3 |
| B lymphocytes CD40L and IL-4 | 24.7 | Dermal fibroblast CCD1070 rest | 59.5 |
| EOL-1 dbcAMP | 12.9 | Dermal fibroblast CCD1070 TNF alpha | 64.2 |
| EOL-1 dbcAMP PMA/ionomycin | 10.4 | Dermal fibroblast CCD1070 IL-1 beta | 32.8 |
| Dendritic cells none | 19.6 | Dermal fibroblast IFN gamma | 10.7 |
| Dendritic cells LPS | 10.7 | Dermal fibroblast IL-4 | 21.6 |
| Dendritic cells anti-CD40 | 18.8 | IBD Colitis 2 | 2.0 |
| Monocytes rest | 15.0 | IBD Crohn's | 3.6 |
| Monocytes LPS | 13.8 | Colon | 36.9 |
| Macrophages rest | 25.3 | Lung | 19.3 |
| Macrophages LPS | 8.1 | Thymus | 72.2 |
| HUVEC none | 19.9 | Kidney | 24.5 |
| HUVEC starved | 35.8 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3380 This panel does not show differential expression of the CG58590-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3380 - This gene is expressed at low to

moderate levels in most tissues. It is also expressed in the skin, heart, lung, liver, and kidney.

Maternal, breast, uterine, lung, ovarian, and prostate cancers. As mentioned above, the expression of this gene could be used as a diagnostic marker for the presence of these cancers.

Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and fetal liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes. Furthermore, this gene is more highly expressed in fetal (CT=30.9) liver when compared to expression in the adult (CT>35) and may be useful for the differentiation of the fetal and adult sources of this tissue.

In addition, this gene is expressed at moderate levels in the all regions of the CNS examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3380 - This gene is expressed from moderate to low levels across all of the samples on this panel. The highest expression is seen in small airway epithelium treated with TNFalpha and IL-1beta (CT=28.7). Interestingly, expression is much lower in untreated small airway epithelium (CT=31.5). There is also a significant difference between mononuclear cells treated with PWM (CT=29.5) and untreated cells (CT=32.7). Therefore, expression of this gene can be used to differentiate treated and untreated samples.

Expression of this gene is detected at a moderate level (CT=30.2) in normal colon (similar levels for colon are seen on panel 1.4 (CT=30.9), but is significantly lower in the IBD Colitis 2 (CT=34.4) and IBD Crohn's (CT=33.5) samples. Therefore, therapies designed with the protein encoded for by this gene may potentially modulate colon function and play a role in the identification and treatment of inflammatory or autoimmune diseases which effect the colon including Crohn's disease and ulcerative colitis.

K. CG58572-01 and CG58572-02: GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE

Table KA. Probe Name Ag3375

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -aagaagtggactggagtcagaa -3' | 22 | 58 | 399 |
| Probe | TET-5'-tacattttctccagccatccccaa-3' TAMRA | 26 | 86 | 400 |
| Reverse | 5' -agcagtacaagaggcctcaa -3' | 21 | 135 | 401 |

Table KB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3375, Run 210154239 | Tissue Name | Rel. Exp.(%) Ag3375, Run 210154239 |
|------------------------|------------------------------------|--------------------------------|------------------------------------|
| AD 1 Hippo | 17.1 | Control (Path) 3 Temporal Ctx | 4.8 |
| AD 2 Hippo | 19.3 | Control (Path) 4 Temporal Ctx | 27.5 |
| AD 3 Hippo | 7.4 | AD 1 Occipital Ctx | 11.5 |
| AD 4 Hippo | 4.5 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 Hippo | 72.2 | AD 3 Occipital Ctx | 5.9 |
| AD 6 Hippo | 53.6 | AD 4 Occipital Ctx | 12.7 |
| Control 2 Hippo | 20.3 | AD 5 Occipital Ctx | 26.6 |
| Control 4 Hippo | 6.8 | AD 6 Occipital Ctx | 19.8 |
| Control (Path) 3 Hippo | 5.5 | Control 1 Occipital Ctx | 3.2 |
| AD 1 Temporal Ctx | 11.6 | Control 2 Occipital Ctx | 36.1 |
| AD 2 Temporal Ctx | 23.8 | Control 3 Occipital Ctx | 7.4 |
| AD 3 Temporal Ctx | 5.5 | Control 4 Occipital Ctx | 4.1 |
| AD 4 Temporal Ctx | 16.5 | Control (Path) 1 Occipital Ctx | 66.0 |
| AD 5 Inf Temporal Ctx | 100.0 | Control (Path) 2 Occipital Ctx | 8.2 |
| AD 5 Sup Temporal Ctx | 55.9 | Control (Path) 3 Occipital Ctx | 1.9 |
| AD 6 Inf Temporal Ctx | 37.9 | Control (Path) 4 Occipital Ctx | 12.2 |

| Sample | Ag3375 | Control 1 Parietal | Control 2 Parietal |
|--------------------|--------|--------------------|--------------------|
| Control 2 Temporal | 25.3 | Control 3 Parietal | 11.7 |

| | | | |
|-------------------------------|------|-------------------------------|------|
| Ctx | | Ctx | |
| Control 3 Temporal Ctx | 8.2 | Control (Path) 1 Parietal Ctx | 49.7 |
| Control 3 Temporal Ctx | 4.0 | Control (Path) 2 Parietal Ctx | 15.4 |
| Control (Path) 1 Temporal Ctx | 52.9 | Control (Path) 3 Parietal Ctx | 4.2 |
| Control (Path) 2 Temporal Ctx | 26.6 | Control (Path) 4 Parietal Ctx | 32.5 |

Table KC. Panel 1.3D

| Tissue Name | Rel. Exp.(%) Ag3375, Run 165674233 | Tissue Name | Rel. Exp.(%) Ag3375, Run 165674233 |
|--------------------------|---------------------------------------|--------------------------------|---------------------------------------|
| Liver adenocarcinoma | 51.8 | Kidney (fetal) | 9.7 |
| Pancreas | 9.3 | Renal ca. 786-0 | 19.6 |
| Pancreatic ca. CAPAN 2 | 52.1 | Renal ca. A498 | 26.2 |
| Adrenal gland | 8.9 | Renal ca. RXF 393 | 15.7 |
| Thyroid | 6.3 | Renal ca. ACHN | 8.2 |
| Salivary gland | 18.3 | Renal ca. UO-31 | 35.4 |
| Pituitary gland | 15.1 | Renal ca. TK-10 | 9.8 |
| Brain (fetal) | 15.5 | Liver | 20.4 |
| Brain (whole) | 34.6 | Liver (fetal) | 16.5 |
| Brain (amygdala) | 16.0 | Liver ca. (hepatoblast) HepG2 | 49.0 |
| Brain (cerebellum) | 34.2 | Lung | 4.5 |
| Brain (hippocampus) | 12.1 | Lung (fetal) | 5.4 |
| Brain (substantia nigra) | 12.8 | Lung ca. (small cell) LX-1 | 32.3 |
| Brain (thalamus) | 17.9 | Lung ca. (small cell) NCI-H69 | 17.3 |
| Cerebral Cortex | 10.4 | Lung ca. (s.cell var.) SHP-77 | 30.1 |
| Spinal cord | 13.3 | Lung ca. (large cell) NCI-H460 | 66.4 |
| glio/astro U87-MG | 14.8 | Lung ca. (non-sm. cell) A549 | 19.1 |
| glio/astro U-118-MG | 95.3 | Lung ca. (non-s.cell) NCI-H23 | 13.8 |

| | | | |
|----------------------------------|-------|--------------------------------|------|
| Astrocytoma SF-539 | 11.4 | Lung ca. (squam.) SW 900 | 9.9 |
| Astrocytoma SNB-75 | 15.6 | Lung ca. (squam.) NCI-H596 | 19.6 |
| glioma SNB-19 | 11.8 | Mammary gland | 14.6 |
| glioma U251 | 40.9 | Breast ca.* (pl.ef) MCF-7 | 81.2 |
| glioma SF-295 | 10.1 | Breast ca.* (pl.ef) MDA-MB-231 | 91.4 |
| Heart (fetal) | 1.3 | Breast ca.* (pl.ef) T47D | 35.4 |
| Heart | 4.7 | Breast ca. BT-549 | 97.9 |
| Skeletal muscle (fetal) | 1.2 | Breast ca. MDA-N | 14.8 |
| Skeletal muscle | 38.7 | Ovary | 1.6 |
| Bone marrow | 4.6 | Ovarian ca. OVCAR-3 | 39.2 |
| Thymus | 2.7 | Ovarian ca. OVCAR-4 | 23.0 |
| Spleen | 7.9 | Ovarian ca. OVCAR-5 | 13.8 |
| Lymph node | 13.0 | Ovarian ca. OVCAR-8 | 8.5 |
| Colorectal | 3.3 | Ovarian ca. IGROV-1 | 5.6 |
| Stomach | 27.7 | Ovarian ca.* (ascites) SK-OV-3 | 44.8 |
| Small intestine | 19.3 | Uterus | 19.5 |
| Colon ca. SW480 | 16.5 | Placenta | 2.6 |
| Colon ca.* SW620(SW480 met) | 29.1 | Prostate | 15.6 |
| Colon ca. HT29 | 13.8 | Prostate ca.* (bone met)PC-3 | 56.6 |
| Colon ca. HCT-116 | 27.7 | Testis | 40.6 |
| Colon ca. CaCo-2 | 17.4 | Melanoma Hs688(A).T | 5.5 |
| Colon ca. tissue(ODO3866) | 26.4 | Melanoma* (met) Hs688(B).T | 8.9 |
| Colon ca. HCC-2998 | 32.1 | Melanoma UACC-62 | 17.8 |
| Gastric ca.* (liver met) NCI-N87 | 100.0 | Melanoma M14 | 27.7 |
| | | Melanoma LOX | |

J. J. JACKMAN

SK-MEL-1

| | | | |
|--------|-----|---------|-----|
| Kidney | 9.0 | Adipose | 8.0 |
|--------|-----|---------|-----|

Table KD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3375, Run 165296547 | Tissue Name | Rel. Exp.(%) Ag3375, Run 165296547 |
|--------------------------------|--|---|--|
| Secondary Th1 act | 14.6 | HUVEC IL-1beta | 24.5 |
| Secondary Th2 act | 13.0 | HUVEC IFN gamma | 24.5 |
| Secondary Tr1 act | 17.3 | HUVEC TNF alpha + IFN gamma | 24.0 |
| Secondary Th1 rest | 0.9 | HUVEC TNF alpha + IL4 | 23.2 |
| Secondary Th2 rest | 1.5 | HUVEC IL-11 | 12.1 |
| Secondary Tr1 rest | 2.9 | Lung Microvascular EC none | 21.3 |
| Primary Th1 act | 16.0 | Lung Microvascular EC TNFalpha + IL-1beta | 24.1 |
| Primary Th2 act | 12.1 | Microvascular Dermal EC none | 27.4 |
| Primary Tr1 act | 25.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 24.0 |
| Primary Th1 rest | 10.4 | Bronchial epithelium TNFalpha + IL1beta | 20.3 |
| Primary Th2 rest | 6.1 | Small airway epithelium none | 11.3 |
| Primary Tr1 rest | 9.0 | Small airway epithelium TNFalpha + IL-1beta | 54.0 |
| CD45RA CD4 lymphocyte act | 14.6 | Coronery artery SMC rest | 23.5 |
| CD45RO CD4 lymphocyte act | 13.6 | Coronery artery SMC TNFalpha + IL-1beta | 12.0 |
| CD8 lymphocyte act | 14.2 | Astrocytes rest | 5.3 |
| Secondary CD8 lymphocyte rest | 14.4 | Astrocytes TNFalpha + IL-1beta | 5.4 |
| Secondary CD8 lymphocyte act | 5.8 | KU-812 (Basophil) rest | 19.5 |
| CD4 lymphocyte none | 2.4 | KU-812 (Basophil) PMA/ionomycin | 56.3 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 2.6 | CCD1106 (Keratinocytes) none | 26.6 |
| LAK cells rest | 5.1 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 7.8 |
| LAK cells IL-2 | 10.7 | Liver cirrhosis | 2.6 |

| | | | |
|-----------------------|------|---------------|------|
| gamma | 16.6 | NCI-H292 IL-4 | 54.7 |
| LAK cells IL-2+ IL-18 | | | |

| | | | |
|-------------------------------|-------|---------------------------------------|------|
| LAK cells PMA/ionomycin | 12.5 | NCI-H292 IL-9 | 45.7 |
| NK Cells IL-2 rest | 7.1 | NCI-H292 IL-13 | 24.3 |
| Two Way MLR 3 day | 6.8 | NCI-H292 IFN gamma | 33.2 |
| Two Way MLR 5 day | 8.9 | HPAEC none | 17.8 |
| Two Way MLR 7 day | 6.0 | HPAEC TNF alpha + IL-1 beta | 30.1 |
| PBMC rest | 0.8 | Lung fibroblast none | 10.2 |
| PBMC PWM | 42.3 | Lung fibroblast TNF alpha + IL-1 beta | 6.3 |
| PBMC PHA-L | 11.6 | Lung fibroblast IL-4 | 27.2 |
| Ramos (B cell) none | 30.6 | Lung fibroblast IL-9 | 26.8 |
| Ramos (B cell) ionomycin | 100.0 | Lung fibroblast IL-13 | 21.8 |
| B lymphocytes PWM | 77.4 | Lung fibroblast IFN gamma | 29.5 |
| B lymphocytes CD40L and IL-4 | 12.2 | Dermal fibroblast CCD1070 rest | 42.3 |
| EOL-1 dbcAMP | 13.0 | Dermal fibroblast CCD1070 TNF alpha | 51.4 |
| EOL-1 dbcAMP PMA/ionomycin | 6.9 | Dermal fibroblast CCD1070 IL-1 beta | 22.5 |
| Dendritic cells none | 4.5 | Dermal fibroblast IFN gamma | 11.1 |
| Dendritic cells LPS | 3.8 | Dermal fibroblast IL-4 | 19.5 |
| Dendritic cells anti-CD40 | 2.9 | IBD Colitis 2 | 0.7 |
| Monocytes rest | 2.2 | IBD Crohn's | 0.9 |
| Monocytes LPS | 1.3 | Colon | 7.6 |
| Macrophages rest | 6.6 | Lung | 6.2 |
| Macrophages LPS | 2.7 | Thymus | 9.4 |
| HUVEC none | 17.4 | Kidney | 4.2 |
| HUVEC starved | 37.4 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3375 This panel does not show differential expression of the CG58572-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

(CI = 28.8). Based on expression in this panel, this gene may be involved in gastric, pancreatic,

brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3375 The CG58572-01 gene is ubiquitously expressed on this panel, with highest expression in the B cell line Ramos treated with ionomycin (CT=26.2). Significant levels of expression are also seen in pokeweed mitogen-activated B lymphocytes. Therefore, therapies that antagonize the function of this gene product may be useful as therapeutic drugs to reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

Interestingly, there is a difference between the levels of expression in resting and activated secondary T cells. The level in activated secondary T cells (CT=28.7-29.2) appears to be higher than in resting T cells (CT=31.3-33.1). Therefore, therapeutics designed with the protein encoded by this transcript could be important in the regulation of T cell function.

L. CG58564-01 and CG58564-02: PROTEIN TYROSINE PHOSPHATASE -

Expression of gene CG58564-01 and full length clone CG58564-02 was assessed using the primer-probe sets Ag3023 and Ag3373, described in Tables LA and LB. Results of the

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-ctaatgctggatttgtccatca-3' | 22 | 492 | 402 |
| Probe | TET-5'-tcaggaatatgaagccatctaccttagca-3' -TAMRA | 28 | 517 | 403 |
| Reverse | 5'-tggagtggtgacatcatctgtca-3' | 22 | 555 | 404 |

Table LB. Probe Name Ag3373

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-atttgcacatcaacttcaggaa-3' | 22 | 502 | 405 |
| Probe | TET-5'-tgaaggccatctaccttagcaaaattaaca-3' -TAMRA | 28 | 526 | 406 |
| Reverse | 5'-tggagtggtgacatcatctgtca-3' | 22 | 555 | 407 |

Table LC. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3023, Run 209821074 | Rel. Exp.(%) Ag3373, Run 210154071 | Tissue Name | Rel. Exp.(%) Ag3023, Run 209821074 | Rel. Exp.(%) Ag3373, Run 210154071 |
|-------------|--|--|-------------------------------|--|--|
| AD 1 Hippo | 10.9 | 16.8 | Control (Path) 3 Temporal Ctx | 9.1 | 8.0 |
| AD 2 Hippo | 34.2 | 37.6 | Control (Path) 4 Temporal Ctx | 40.6 | 65.5 |
| AD 3 Hippo | 12.0 | 15.8 | AD 1 Occipital Ctx | 24.7 | 29.1 |
| AD 4 Hippo | 13.8 | 10.3 | AD 2 Occipital Ctx (Missing) | 0.0 | 0.0 |
| AD 5 hippo | 60.7 | 57.8 | AD 3 Occipital Ctx | 14.7 | 15.0 |
| AD 6 Hippo | 80.7 | 72.2 | AD 4 Occipital Ctx | 35.4 | 22.4 |

| | | | | | |
|-----------|------|-----|------|------|------|
| Control 4 | 16.5 | ... | AD 6 | 46.3 | 55.4 |
|-----------|------|-----|------|------|------|

| | | | | | |
|----------------------------|-------|-------|---|------|------|
| Hippo | | | Occipital Ctx | | |
| Control (Path) 3 Hippo | 13.1 | 15.4 | Control 1 Occipital Ctx | 9.9 | 10.7 |
| AD 1 Temporal Ctx | 39.0 | 31.4 | Control 2 Occipital Ctx | 39.0 | 38.4 |
| AD 2 Temporal Ctx | 38.7 | 73.2 | Control 3 Occipital Ctx | 23.0 | 20.6 |
| AD 3 Temporal Ctx | 9.5 | 13.2 | Control 4 Occipital Ctx | 13.3 | 13.3 |
| AD 4 Temporal Ctx | 27.9 | 34.9 | Control (Path) 1 Occipital Ctx | 80.1 | 76.3 |
| AD 5 Inf Temporal Ctx | 59.0 | 100.0 | Control (Path) 2 Occipital Ctx | 17.3 | 20.0 |
| AD 5 SupTemporal Ctx | 33.2 | 44.1 | Control (Path) 3 Occipital Ctx | 8.4 | 8.7 |
| AD 6 Inf Temporal Ctx | 100.0 | 73.2 | Control (Path) 4 Occipital Ctx | 21.2 | 20.6 |
| AD 6 Sup Temporal Ctx | 79.6 | 80.1 | Control 1 Parietal Ctx | 12.1 | 16.3 |
| Control 1 Temporal Ctx | 10.2 | 13.7 | Control 2 Parietal Ctx | 48.0 | 40.9 |
| Control 2 Temporal Ctx | 41.2 | 31.9 | Control 3 Parietal Ctx | 17.9 | 16.3 |
| Control 3 Temporal Ctx | 20.3 | 20.0 | Control (Path) 1 Parietal Ctx | 74.7 | 64.2 |
| Control 4 Temporal Ctx | 9.7 | 9.9 | Control (Path) 2 Parietal Ctx | 28.9 | 59.9 |
| Control 5 Temporal Ctx | | | Control | | |

| Control (Path) 2 Temporal Ctx | 44.2 | 44.2 | Control (Path) 4 | 44.8 | 43.8 |
|----------------------------------|------|------|---------------------|------|------|
| | | | | | |

| | | | |
|--|--|--------------|--|
| | | Parietal Ctx | |
|--|--|--------------|--|

Table LD. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3373, Run 217043119 | Tissue Name | Rel. Exp.(%) Ag3373, Run 217043119 |
|-------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 12.0 | Renal ca. TK-10 | 20.3 |
| Melanoma* Hs688(A).T | 30.8 | Bladder | 23.2 |
| Melanoma* Hs688(B).T | 69.3 | Gastric ca. (liver met.) NCI-N87 | 25.3 |
| Melanoma* M14 | 15.0 | Gastric ca. KATO III | 30.8 |
| Melanoma* LOXIMVI | 26.6 | Colon ca. SW-948 | 9.7 |
| Melanoma* SK-MEL-5 | 21.5 | Colon ca. SW480 | 35.1 |
| Squamous cell carcinoma SCC-4 | 33.0 | Colon ca.* (SW480 met) SW620 | 13.9 |
| Testis Pool | 19.8 | Colon ca. HT29 | 8.5 |
| Prostate ca.* (bone met) PC-3 | 100.0 | Colon ca. HCT-116 | 36.9 |
| Prostate Pool | 9.2 | Colon ca. CaCo-2 | 42.9 |
| Placenta | 3.8 | Colon cancer tissue | 9.0 |
| Uterus Pool | 7.4 | Colon ca. SW1116 | 5.8 |
| Ovarian ca. OVCAR-3 | 28.5 | Colon ca. Colo-205 | 4.3 |
| Ovarian ca. SK-OV-3 | 40.3 | Colon ca. SW-48 | 4.2 |
| Ovarian ca. OVCAR-4 | 20.0 | Colon Pool | 20.7 |
| Ovarian ca. OVCAR-5 | 35.1 | Small Intestine Pool | 12.2 |
| Ovarian ca. IGROV-1 | 10.9 | Stomach Pool | 9.9 |
| Ovarian ca. OVCAR-8 | 9.2 | Bone Marrow Pool | 11.6 |
| Ovary | 9.7 | Fetal Heart | 20.7 |
| Breast ca. MCF-7 | 37.6 | Heart Pool | 10.6 |
| Breast ca. MDA-MB-231 | 37.1 | Lymph Node Pool | 17.9 |

| | | | |
|-----------------------|------|-------------|------|
| Breast ca. MDA-MB-231 | 17.3 | Spleen Pool | 12.2 |
| Breast Pool | | Thymus Pool | |

| | | | |
|-------------------|------|-------------------------------------|------|
| Trachea | 12.0 | CNS cancer (glio/astro) U87-MG | 29.1 |
| Lung | 6.7 | CNS cancer (glio/astro) U-118-MG | 69.3 |
| Fetal Lung | 34.2 | CNS cancer (neuro;met) SK-N-AS | 34.9 |
| Lung ca. NCI-N417 | 5.4 | CNS cancer (astro) SF-539 | 19.1 |
| Lung ca. LX-1 | 17.2 | CNS cancer (astro) SNB-75 | 35.8 |
| Lung ca. NCI-H146 | 3.0 | CNS cancer (glio) SNB-19 | 11.3 |
| Lung ca. SHP-77 | 18.6 | CNS cancer (glio) SF-295 | 26.4 |
| Lung ca. A549 | 29.1 | Brain (Amygdala) Pool | 4.5 |
| Lung ca. NCI-H526 | 4.6 | Brain (cerebellum) | 8.1 |
| Lung ca. NCI-H23 | 31.6 | Brain (fetal) | 13.2 |
| Lung ca. NCI-H460 | 18.2 | Brain (Hippocampus) Pool | 5.3 |
| Lung ca. HOP-62 | 14.1 | Cerebral Cortex Pool | 5.4 |
| Lung ca. NCI-H522 | 31.6 | Brain (Substantia nigra) Pool | 4.8 |
| Liver | 1.2 | Brain (Thalamus) Pool | 8.0 |
| Fetal Liver | 32.3 | Brain (whole) | 6.2 |
| Liver ca. HepG2 | 14.6 | Spinal Cord Pool | 6.6 |
| Kidney Pool | 22.1 | Adrenal Gland | 8.1 |
| Fetal Kidney | 26.1 | Pituitary gland Pool | 3.0 |
| Renal ca. 786-0 | 28.7 | Salivary Gland | 4.7 |
| Renal ca. A498 | 11.3 | Thyroid (female) | 4.4 |
| Renal ca. ACHN | 12.2 | Pancreatic ca. CAPAN2 | 17.3 |
| Renal ca. UO-31 | 24.1 | Pancreas Pool | 17.1 |

Table LE. Panel 1.3D

| Tissue Name | Rel. Exp.(%) Ag3023, Run 167966931 | Tissue Name | Rel. Exp.(%) Ag3023, Run 167966931 |
|-----------------------|---------------------------------------|-----------------|---------------------------------------|
| Liver adenocarcinoma | 51.1 | Kidney (fetal) | 26.2 |
| Pancreas | 6.1 | Renal ca. 786-0 | 34.2 |
| Pancreatic ca. CAPAN2 | 17.7 | Renal ca. A498 | 17.6 |

Salivary gland

Renal ca. UO-31

| | | | |
|--------------------------|------|-----------------------------------|------|
| Pituitary gland | 3.6 | Renal ca. TK-10 | 23.0 |
| Brain (fetal) | 8.1 | Liver | 11.7 |
| Brain (whole) | 8.5 | Liver (fetal) | 8.0 |
| Brain (amygdala) | 6.7 | Liver ca. (hepatoblast) HepG2 | 26.2 |
| Brain (cerebellum) | 15.2 | Lung | 3.1 |
| Brain (hippocampus) | 5.4 | Lung (fetal) | 11.0 |
| Brain (substantia nigra) | 9.0 | Lung ca. (small cell) LX-1 | 12.9 |
| Brain (thalamus) | 4.2 | Lung ca. (small cell) NCI-H69 | 9.9 |
| Cerebral Cortex | 2.0 | Lung ca. (s.cell var.) SHP-77 | 67.8 |
| Spinal cord | 6.9 | Lung ca. (large cell)NCI-H460 | 3.4 |
| glio/astro U87-MG | 28.5 | Lung ca. (non-sm. cell) A549 | 45.1 |
| glio/astro U-118-MG | 46.7 | Lung ca. (non-s.cell) NCI-H23 | 22.7 |
| astrocytoma SW1783 | 40.6 | Lung ca. (non-s.cell) HOP-62 | 25.7 |
| neuro*; met SK-N-AS | 27.2 | Lung ca. (non-s.cl) NCI-H522 | 38.2 |
| astrocytoma SF-539 | 29.7 | Lung ca. (squam.) SW 900 | 27.4 |
| astrocytoma SNB-75 | 35.1 | Lung ca. (squam.) NCI-H596 | 29.9 |
| glioma SNB-19 | 15.6 | Mammary gland | 5.1 |
| glioma U251 | 37.9 | Breast ca.* (pl.ef) MCF-7 | 47.0 |
| glioma SF-295 | 18.4 | Breast ca.* (pl.ef) MDA-MB-231 | 22.7 |
| Heart (fetal) | 2.9 | Breast ca.* (pl.ef) T47D | 86.5 |
| Heart | 12.9 | Breast ca. BT-549 | 15.9 |
| Skeletal muscle (fetal) | 3.4 | Breast ca. MDA-N | 10.4 |
| Skeletal muscle | 36.3 | Ovary | 2.9 |
| Bone marrow | 4.5 | Ovarian ca. OVCAR- 3 | 26.1 |
| Thymus | 14.3 | Ovarian ca. OVCAR- 4 | 16.3 |

| | | | |
|------------|------|---------------------|-----|
| Lymph node | 11.8 | Ovarian ca. OVCAR-8 | 9.5 |
|------------|------|---------------------|-----|

| | | | |
|-------------------------------------|------|-----------------------------------|-------|
| Colorectal | 10.4 | Ovarian ca. IGROV-1 | 12.0 |
| Stomach | 7.8 | Ovarian ca.* (ascites) SK-OV-3 | 100.0 |
| Small intestine | 5.1 | Uterus | 4.9 |
| Colon ca. SW480 | 19.3 | Placenta | 1.3 |
| Colon ca.* SW620(SW480 met) | 42.9 | Prostate | 3.9 |
| Colon ca. HT29 | 9.9 | Prostate ca.* (bone met)PC-3 | 78.5 |
| Colon ca. HCT-116 | 26.2 | Testis | 9.7 |
| Colon ca. CaCo-2 | 41.5 | Melanoma Hs688(A).T | 5.9 |
| Colon ca. tissue(ODO3866) | 6.3 | Melanoma* (met) Hs688(B).T | 14.2 |
| Colon ca. HCC-2998 | 16.0 | Melanoma UACC-62 | 14.0 |
| Gastric ca.* (liver met) NCI-N87 | 18.8 | Melanoma M14 | 5.7 |
| Bladder | 30.6 | Melanoma LOX IMVI | 8.8 |
| Trachea | 3.2 | Melanoma* (met) SK-MEL-5 | 14.7 |
| Kidney | 9.6 | Adipose | 18.9 |

Table LF. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3023, Run 164516146 | Rel. Exp.(%) Ag3373, Run 165296617 | Tissue Name | Rel. Exp.(%) Ag3023, Run 164516146 | Rel. Exp.(%) Ag3373, Run 165296617 |
|--------------------|---|---|-----------------------------------|---|---|
| Secondary Th1 act | 18.6 | 17.9 | HUVEC IL-1beta | 20.3 | 18.6 |
| Secondary Th2 act | 24.3 | 28.5 | HUVEC IFN gamma | 25.3 | 22.7 |
| Secondary Tr1 act | 22.8 | 21.8 | HUVEC TNF alpha + IFN gamma | 16.3 | 18.0 |
| Secondary Th1 rest | 7.5 | 6.8 | HUVEC TNF alpha + IL4 | 18.2 | 13.4 |
| Secondary Th2 rest | 11.6 | 9.5 | HUVEC IL-11 | 13.7 | 9.9 |
| | | | Lung | | |

| | | | | |
|-----------------|-----|------|------------------|-----|
| Primary Th1 act | 100 | lung | Microvascular EC | 100 |
| | | | | |

| | | | | | |
|---------------------------------------|------|------|---|------|------|
| | | | TNFalpha + IL-1beta | | |
| Primary Th2 act | 20.2 | 19.3 | Microvascular Dermal EC none | 27.5 | 21.3 |
| Primary Tr1 act | 23.3 | 27.7 | Microvasular Dermal EC TNFalpha + IL-1beta | 20.7 | 19.9 |
| Primary Th1 rest | 51.1 | 51.4 | Bronchial epithelium TNFalpha + IL1beta | 13.0 | 16.3 |
| Primary Th2 rest | 26.2 | 29.5 | Small airway epithelium none | 8.1 | 8.5 |
| Primary Tr1 rest | 23.7 | 26.1 | Small airway epithelium TNFalpha + IL-1beta | 50.3 | 39.8 |
| CD45RA CD4 lymphocyte act | 14.6 | 11.0 | Coronery artery SMC rest | 20.2 | 18.9 |
| CD45RO CD4 lymphocyte act | 25.2 | 22.4 | Coronery artery SMC TNFalpha + IL-1beta | 12.0 | 9.8 |
| CD8 lymphocyte act | 20.4 | 15.8 | Astrocytes rest | 10.4 | 11.1 |
| Secondary CD8 lymphocyte rest | 16.5 | 19.9 | Astrocytes TNFalpha + IL-1beta | 11.7 | 9.8 |
| Secondary CD8 lymphocyte act | 13.2 | 9.3 | KU-812 (Basophil) rest | 47.6 | 38.2 |
| CD4 lymphocyte none | 17.1 | 11.6 | KU-812 (Basophil) PMA/ionomycin | 94.0 | 92.0 |
| 2ry Th1/Th2/Tr1_anti- CD95 CH11 | 18.3 | 16.6 | CCD1106 (Keratinocytes) none | 19.9 | 13.2 |
| LAK cells rest | 25.5 | 16.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 6.0 | 4.8 |
| LAK cells IL-2 | 27.2 | 22.5 | Liver cirrhosis | 3.1 | 2.7 |
| LAK cells IL-2+IL-12 | 27.2 | 19.3 | Lupus kidney | 2.1 | 1.7 |

| | | | | | |
|-------------------------|------|------|---------------|------|------|
| LAK cells IL-2 IL-18 | 35.1 | 29.7 | NCI-H292 IL-4 | 33.9 | 34.6 |
|-------------------------|------|------|---------------|------|------|

| | | | | | |
|---------------------------------|-------|-------|---------------------------------------|------|------|
| LAK cells PMA/ionomycin | 12.4 | 11.0 | NCI-H292 IL-9 | 40.1 | 29.1 |
| NK Cells IL-2 rest | 20.0 | 15.0 | NCI-H292 IL-13 | 16.2 | 14.2 |
| Two Way MLR 3 day | 24.0 | 16.7 | NCI-H292 IFN gamma | 16.6 | 18.4 |
| Two Way MLR 5 day | 12.9 | 10.1 | HPAEC none | 13.6 | 13.5 |
| Two Way MLR 7 day | 11.4 | 9.5 | HPAEC TNF alpha + IL-1 beta | 25.3 | 25.3 |
| PBMC rest | 13.7 | 10.5 | Lung fibroblast none | 11.4 | 14.2 |
| PBMC PWM | 69.3 | 66.4 | Lung fibroblast TNF alpha + IL-1 beta | 6.1 | 7.2 |
| PBMC PHA-L | 22.8 | 17.7 | Lung fibroblast IL-4 | 28.5 | 29.1 |
| Ramos (B cell) none | 24.1 | 19.3 | Lung fibroblast IL-9 | 23.0 | 23.3 |
| Ramos (B cell) ionomycin | 100.0 | 100.0 | Lung fibroblast IL-13 | 20.6 | 18.9 |
| B lymphocytes PWM | 71.7 | 74.2 | Lung fibroblast IFN gamma | 39.0 | 32.5 |
| B lymphocytes CD40L and IL-4 | 29.1 | 28.7 | Dermal fibroblast CCD1070 rest | 33.9 | 31.0 |
| EOL-1 dbcAMP | 12.1 | 10.5 | Dermal fibroblast CCD1070 TNF alpha | 76.8 | 62.0 |
| EOL-1 dbcAMP PMA/ionomycin | 14.5 | 10.9 | Dermal fibroblast CCD1070 IL-1 beta | 20.3 | 13.9 |
| Dendritic cells none | 13.2 | 14.8 | Dermal fibroblast IFN gamma | 14.2 | 9.5 |
| Dendritic cells LPS | 11.7 | 8.3 | Dermal fibroblast IL-4 | 26.4 | 20.4 |
| Dendritic cells anti- CD40 | 17.7 | 12.7 | IBD Colitis 2 | 2.6 | 2.2 |
| Monocytes rest | 16.7 | 17.6 | IBD Crohn's | 2.0 | 1.9 |
| Monocytes LPS | 6.4 | 5.0 | Colon | 11.9 | 10.5 |
| Macrophages rest | 23.5 | 22.8 | Lung | 13.3 | 11.2 |
| Macrophages LPS | 9.9 | 7.1 | Thymus | 14.4 | 12.9 |
| HUVEC none | 20.6 | 17.9 | Kidney | 27.5 | 19.6 |

NS neurodegeneration v1.0 Summary. This table summarizes the differential expression of the CG58564-01 gene in Alzheimer's disease. However, this

expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General screening panel v1.4 Summary: Ag3373 Highest expression of the CG58564-01 gene is seen in a prostate cancer cell line (CT=27). Overall, this gene is expressed at moderate levels in the cancer cell lines in this panel. A higher level of expression is observed in clusters of cell lines derived from prostate, brain, melanoma, colon, lung, breast and ovarian cancer when compared to expression in normal prostate, brain, colon, lung, breast and ovary. Thus, this gene could potentially be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, this gene product has moderate levels of expression in adipose, heart, skeletal muscle, adrenal, pituitary, thyroid and pancreas. Thus, this gene product may be a small molecule target for the treatment of endocrine and metabolic diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene appears to be differentially expressed in fetal (CT value = 29) vs adult liver (CT value =33) and may be useful for differentiation between the two sources of this tissue.

This gene is also expressed at moderate levels in all central nervous system samples present on this panel. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

Panel 1.3D Summary: Ag3023 The CG58564-01 gene is ubiquitously expressed among the samples on this panel, with highest expression in an ovarian cancer cell line (CT=28.8). Overall, the expression of this gene shows good agreement with panel 1.4. A higher level of expression is observed in prostate, brain, melanoma, colon, lung, pancreatic, breast and ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and ovary. Thus, expression of this gene could be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

previous panel. Please see Panel 1.4 for discussion of utility of this gene in metabolic disease.

This gene represents a phosphatase that is also expressed at low to moderate levels across the CNS. Some phosphatases comprise a family of MAP kinase regulating enzymes, members of which are upregulated in brains subjected to insults such as ischemia and seizure activity. MAP kinases are known to regulate neurotrophic and neurotoxic pathways. Consequently, agents that modulate the activity of this gene may have utility in attenuating the apoptotic and neurodegenerative processes following brain insults.

References:

1. Wiessner C. The dual specificity phosphatase PAC-1 is transcriptionally induced in the rat brain following transient forebrain ischemia. *Brain Res Mol Brain Res* 1995 Feb;28(2):353-6
2. Boschert U, Muda M, Camps M, Dickinson R, Arkinstall S. Induction of the dual specificity phosphatase PAC1 in rat brain following seizure activity. *Neuroreport* 1997 Sep 29;8(14):3077-80

Panel 4D Summary: Ag3023/Ag3373 The CG585864-01 gene is expressed at high to moderate levels in a wide range of cell types and tissues of significance in the immune response in health and disease. Highest expression of this gene is seen in ionomycin treated Ramos B cells (CT=26.83). Therefore, targeting of this gene product with a small molecule drug or antibody therapeutic may modulate the functions of cells of the immune system as well as resident tissue cells and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, and arthritis, including osteoarthritis and rheumatoid arthritis.

M. CG58564-03: Dual specificity phosphatase

Expression of gene CG58564-03 was assessed using the primer-probe sets Ag3023, Ag3373 and Ag5847, described in Tables MA, MB and MC. Results of the RTQ-PCR runs are shown in Tables MD, ME, MF, MG and MH.

Table MA. Probe Name Ag3023

| Forward | Sequence | POSITION | SC |
|---------|---------------------|----------------|----|
| | ttatgttgttttgtccata | 22 261 408 | |

| | | | | |
|---------|--|----|-----|-----|
| Probe | TET-5'-tcaggaatatgaagccatctacctagca- 3'-TAMRA | 28 | 230 | 409 |
| Reverse | 5'-tggagtggtgacatcatctgta-3' | 22 | 198 | 410 |

Table MB. Probe Name Ag3373

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-atttgtccatcaacttcaggaa-3' | 22 | 251 | 411 |
| Probe | TET-5'-tgaagccatctacacctagaaaattaaca- 3'-TAMRA | 28 | 221 | 412 |
| Reverse | 5'-tggagtggtgacatcatctgta-3' | 22 | 198 | 413 |

Table MC. Probe Name Ag5847

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-cattccaaatgtttctgtagt-3' | 21 | 335 | 414 |
| Probe | TET-5'-ttcatagcagatgaatatgggcctaagaac- 3'-TAMRA | 30 | 371 | 415 |
| Reverse | 5'-ccacagtgcaggaagac-3' | 18 | 457 | 416 |

Table MD. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3023, Run 209821074 | Rel. Exp.(%) Ag3373, Run 210154071 | Tissue Name | Rel. Exp.(%) Ag3023, Run 209821074 | Rel. Exp.(%) Ag3373, Run 210154071 |
|-------------|--|--|--|--|--|
| AD 1 Hippo | 10.9 | 16.8 | Control (Path) 3 Temporal Ctx | 9.1 | 8.0 |
| AD 2 Hippo | 34.2 | 37.6 | Control (Path) 4 Temporal Ctx | 40.6 | 65.5 |
| AD 3 Hippo | 12.0 | 15.8 | AD 1 Occipital Ctx | 24.7 | 29.1 |
| AD 4 Hippo | 13.8 | 10.3 | AD 2 Occipital Ctx (Missing) | 0.0 | 0.0 |

| | | | | | |
|------------|------|------|------|------|------|
| AD 6 Hippo | 80.7 | 72.2 | AD 4 | 35.4 | 22.4 |
|------------|------|------|------|------|------|

| | | | Occipital Ctx | | |
|----------------------------|-------|-------|---|------|------|
| Control 2 Hippo | 35.8 | 38.4 | AD 5 Occipital Ctx | 3.9 | 30.4 |
| Control 4 Hippo | 16.5 | 11.7 | AD 6 Occipital Ctx | 46.0 | 37.4 |
| Control (Path) 3 Hippo | 13.1 | 15.4 | Control 1 Occipital Ctx | 9.9 | 10.7 |
| AD 1 Temporal Ctx | 39.0 | 31.4 | Control 2 Occipital Ctx | 39.0 | 38.4 |
| AD 2 Temporal Ctx | 38.7 | 73.2 | Control 3 Occipital Ctx | 23.0 | 20.6 |
| AD 3 Temporal Ctx | 9.5 | 13.2 | Control 4 Occipital Ctx | 13.3 | 13.3 |
| AD 4 Temporal Ctx | 27.9 | 34.9 | Control (Path) 1 Occipital Ctx | 80.1 | 76.3 |
| AD 5 Inf Temporal Ctx | 59.0 | 100.0 | Control (Path) 2 Occipital Ctx | 17.3 | 20.0 |
| AD 5 SupTemporal Ctx | 33.2 | 44.1 | Control (Path) 3 Occipital Ctx | 8.4 | 8.7 |
| AD 6 Inf Temporal Ctx | 100.0 | 73.2 | Control (Path) 4 Occipital Ctx | 21.2 | 20.6 |
| AD 6 Sup Temporal Ctx | 79.6 | 80.1 | Control 1 Parietal Ctx | 12.1 | 16.3 |
| Control 1 Temporal Ctx | 10.2 | 13.7 | Control 2 Parietal Ctx | 48.0 | 40.9 |
| Control 2 Temporal Ctx | 41.2 | 31.9 | Control 3 Parietal Ctx | 17.9 | 16.3 |

Control

| Temporal Ctx | 3.9 | 9.9 | Control (Path) 2 | 28.9 | 39.9 |
|--------------|-----|-----|---------------------|------|------|
| | | | | | |

| | | | | | |
|----------------------------------|------|------|-------------------------------------|------|------|
| | | | Parietal Ctx | | |
| Control (Path) 1 Temporal Ctx | 59.9 | 68.3 | Control (Path) 3 Parietal Ctx | 10.2 | 9.0 |
| Control (Path) 2 Temporal Ctx | 40.3 | 41.2 | Control (Path) 4 Parietal Ctx | 44.8 | 43.8 |

Table ME. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3373, Run 217043119 | Tissue Name | Rel. Exp.(%) Ag3373, Run 217043119 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 12.0 | Renal ca. TK-10 | 20.3 |
| Melanoma* Hs688(A).T | 30.8 | Bladder | 23.2 |
| Melanoma* Hs688(B).T | 69.3 | Gastric ca. (liver met.) NCI-N87 | 25.3 |
| Melanoma* M14 | 15.0 | Gastric ca. KATO III | 30.8 |
| Melanoma* LOXIMVI | 26.6 | Colon ca. SW-948 | 9.7 |
| Melanoma* SK- MEL-5 | 21.5 | Colon ca. SW480 | 35.1 |
| Squamous cell carcinoma SCC-4 | 33.0 | Colon ca.* (SW480 met) SW620 | 13.9 |
| Testis Pool | 19.8 | Colon ca. HT29 | 8.5 |
| Prostate ca.* (bone met) PC-3 | 100.0 | Colon ca. HCT-116 | 36.9 |
| Prostate Pool | 9.2 | Colon ca. CaCo-2 | 42.9 |
| Placenta | 3.8 | Colon cancer tissue | 9.0 |
| Uterus Pool | 7.4 | Colon ca. SW1116 | 5.8 |
| Ovarian ca. OVCAR-3 | 28.5 | Colon ca. Colo-205 | 4.3 |
| Ovarian ca. SK-OV- 3 | 40.3 | Colon ca. SW-48 | 4.2 |
| Ovarian ca. OVCAR-4 | 20.0 | Colon Pool | 20.7 |
| Ovarian ca. OVCAR-5 | 35.1 | Small Intestine Pool | 12.2 |
| Ovarian ca. IGROV- 1 | 10.9 | Stomach Pool | 9.9 |
| Ovarian ca. | | | |

| | | | |
|-----------------|------|-----------------|------|
| Breast ca. MCF- | 87.6 | Heart Pool | 10.6 |
| Breast ca. MDA- | 37.1 | Lymph Node Pool | 17.9 |

| | | | |
|-------------------|------|-------------------------------------|------|
| MB-231 | | | |
| Breast ca. BT 549 | 62.4 | Fetal Skeletal Muscle | 12.3 |
| Breast ca. T47D | 61.1 | Skeletal Muscle Pool | 16.0 |
| Breast ca. MDA-N | 10.0 | Spleen Pool | 11.6 |
| Breast Pool | 17.3 | Thymus Pool | 12.2 |
| Trachea | 12.0 | CNS cancer (glio/astro) U87-MG | 29.1 |
| Lung | 6.7 | CNS cancer (glio/astro) U-118-MG | 69.3 |
| Fetal Lung | 34.2 | CNS cancer (neuro;met) SK-N-AS | 34.9 |
| Lung ca. NCI-N417 | 5.4 | CNS cancer (astro) SF- 539 | 19.1 |
| Lung ca. LX-1 | 17.2 | CNS cancer (astro) SNB-75 | 35.8 |
| Lung ca. NCI-H146 | 3.0 | CNS cancer (glio) SNB-19 | 11.3 |
| Lung ca. SHP-77 | 18.6 | CNS cancer (glio) SF- 295 | 26.4 |
| Lung ca. A549 | 29.1 | Brain (Amygdala) Pool | 4.5 |
| Lung ca. NCI-H526 | 4.6 | Brain (cerebellum) | 8.1 |
| Lung ca. NCI-H23 | 31.6 | Brain (fetal) | 13.2 |
| Lung ca. NCI-H460 | 18.2 | Brain (Hippocampus) Pool | 5.3 |
| Lung ca. HOP-62 | 14.1 | Cerebral Cortex Pool | 5.4 |
| Lung ca. NCI-H522 | 31.6 | Brain (Substantia nigra) Pool | 4.8 |
| Liver | 1.2 | Brain (Thalamus) Pool | 8.0 |
| Fetal Liver | 32.3 | Brain (whole) | 6.2 |
| Liver ca. HepG2 | 14.6 | Spinal Cord Pool | 6.6 |
| Kidney Pool | 22.1 | Adrenal Gland | 8.1 |
| Fetal Kidney | 26.1 | Pituitary gland Pool | 3.0 |
| Renal ca. 786-0 | 28.7 | Salivary Gland | 4.7 |
| Renal ca. A498 | 11.3 | Thyroid (female) | 4.4 |
| Renal ca. ACHN | 12.2 | Pancreatic ca. CAPAN2 | 17.3 |
| Renal ca. UO-31 | 24.1 | Pancreas Pool | 17.1 |

Table MF_General_screening_panel_v1.5

| Dose response curves | | Dose response curves | |
|----------------------|-------|----------------------|-------|
| Antigen | Conc. | Antigen | Conc. |
| Melanoma* | 0.1 | Bladder | 0.1 |

| | | | |
|-------------------------------|-----|-------------------------------------|-----|
| Hs688(A).T | | | |
| Melanoma* | 0.1 | Gastric ca. (liver met.) NCI-N87 | 0.2 |
| Hs688(B).T | | | |
| Melanoma* M14 | 0.1 | Gastric ca. KATO III | 0.1 |
| Melanoma* LOXIMVI | 0.1 | Colon ca. SW-948 | 0.1 |
| Melanoma* SK-MEL-5 | 0.1 | Colon ca. SW480 | 0.2 |
| Squamous cell carcinoma SCC-4 | 0.2 | Colon ca.* (SW480 met) SW620 | 1.8 |
| Testis Pool | 0.1 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.6 | Colon ca. HCT-116 | 0.2 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 0.0 |
| Placenta | 0.0 | Colon cancer tissue | 0.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.2 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.1 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.1 | Colon Pool | 0.1 |
| Ovarian ca. OVCAR-5 | 0.2 | Small Intestine Pool | 0.0 |
| Ovarian ca. IGROV-1 | 0.0 | Stomach Pool | 0.0 |
| Ovarian ca. OVCAR-8 | 0.1 | Bone Marrow Pool | 0.0 |
| Ovary | 0.1 | Fetal Heart | 0.1 |
| Breast ca. MCF-7 | 0.3 | Heart Pool | 0.0 |
| Breast ca. MDA-MB-231 | 0.2 | Lymph Node Pool | 0.1 |
| Breast ca. BT 549 | 0.2 | Fetal Skeletal Muscle | 0.1 |
| Breast ca. T47D | 0.2 | Skeletal Muscle Pool | 0.1 |
| Breast ca. MDA-N | 0.1 | Spleen Pool | 0.1 |
| Breast Pool | 0.0 | Thymus Pool | 0.1 |
| Trachea | 0.1 | CNS cancer (glio/astro) U87-MG | 0.2 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.5 |

| | | | |
|-------------------|-----|----------------------------------|--------------|
| Lung ca. LX-1 | 0.0 | CNS cancer (astro) SNB-75 | 0.2 |
| Lung ca. NCI-H146 | 0.0 | CNS cancer (glio) SNB-19 | 0.1 |
| Lung ca. SHP-77 | 0.1 | CNS cancer (glio) SF-295 | 0.2 |
| Lung ca. A549 | 0.2 | Brain (Amygdala) Pool | 0.0 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 0.0 |
| Lung ca. NCI-H23 | 0.1 | Brain (fetal) | 0.1 |
| Lung ca. NCI-H460 | 0.1 | Brain (Hippocampus) Pool | 0.0 |
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 0.0 |
| Lung ca. NCI-H522 | 0.1 | Brain (Substantia nigra) Pool | 0.0 |
| Liver | 0.0 | Brain (Thalamus) Pool | 0.0 |
| Fetal Liver | 0.1 | Brain (whole) | 0.0 |
| Liver ca. HepG2 | 0.1 | Spinal Cord Pool | 0.0 |
| Kidney Pool | 0.1 | Adrenal Gland | 0.0 |
| Fetal Kidney | 0.1 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 0.2 | Salivary Gland | 100.0 |
| Renal ca. A498 | 0.1 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 0.1 | Pancreatic ca. CAPAN2 | 0.1 |
| Renal ca. UO-31 | 0.1 | Pancreas Pool | 0.0 |

Table MG. Panel 1.3D

| Tissue Name | Rel. Exp.(%) Ag3023, Run 167966931 | Tissue Name | Rel. Exp.(%) Ag3023, Run 167966931 |
|---------------------------|---------------------------------------|-------------------|---------------------------------------|
| Liver adenocarcinoma | 51.1 | Kidney (fetal) | 26.2 |
| Pancreas | 6.1 | Renal ca. 786-0 | 34.2 |
| Pancreatic ca. CAPAN 2 | 17.7 | Renal ca. A498 | 17.6 |
| Adrenal gland | 3.8 | Renal ca. RXF 393 | 17.2 |
| Thyroid | 3.0 | Renal ca. ACHN | 13.5 |
| Salivary gland | 3.9 | Renal ca. UO-31 | 0.0 |
| Pituitary gland | 3.6 | Renal ca. TK-10 | 23.0 |
| Brain (fetal) | 8.1 | Liver | 11.7 |
| Brain (whole) | 8.5 | Liver (fetal) | 8.0 |
| Brain (hippocampus) | — | Liver ca. | 26.2 |

| | | | |
|--------------------------|-----|-----------------------|------|
| Brain (hippocampus) | — | Lung (fetal) | — |
| Brain (substantia nigra) | 9.0 | Lung ca. (small cell) | 12.9 |

| | | | |
|-------------------------|------|-----------------------------------|-------|
| | | LX-1 | |
| Brain (thalamus) | 4.2 | Lung ca. (small cell) NCI-H69 | 9.9 |
| Cerebral Cortex | 2.0 | Lung ca. (s.cell var.) SHP-77 | 67.8 |
| Spinal cord | 6.9 | Lung ca. (large cell)NCI-H460 | 3.4 |
| Glio/astro U87-MG | 28.5 | Lung ca. (non-sm. cell) A549 | 45.1 |
| Glio/astro U-118-MG | 46.7 | Lung ca. (non-s.cell) NCI-H23 | 22.7 |
| astrocytoma SW1783 | 40.6 | Lung ca. (non-s.cell) HOP-62 | 25.7 |
| neuro*, met SK-N-AS | 27.2 | Lung ca. (non-s.cl) NCI-H522 | 38.2 |
| astrocytoma SF-539 | 29.7 | Lung ca. (squam.) SW 900 | 27.4 |
| astrocytoma SNB-75 | 35.1 | Lung ca. (squam.) NCI-H596 | 29.9 |
| glioma SNB-19 | 15.6 | Mammary gland | 5.1 |
| glioma U251 | 37.9 | Breast ca.* (pl.ef) MCF-7 | 47.0 |
| glioma SF-295 | 18.4 | Breast ca.* (pl.ef) MDA-MB-231 | 22.7 |
| Heart (fetal) | 2.9 | Breast ca.* (pl.ef) T47D | 86.5 |
| Heart | 12.9 | Breast ca. BT-549 | 15.9 |
| Skeletal muscle (fetal) | 3.4 | Breast ca. MDA-N | 10.4 |
| Skeletal muscle | 36.3 | Ovary | 2.9 |
| Bone marrow | 4.5 | Ovarian ca. OVCAR- 3 | 26.1 |
| Thymus | 14.3 | Ovarian ca. OVCAR- 4 | 16.3 |
| Spleen | 8.7 | Ovarian ca. OVCAR- 5 | 83.5 |
| Lymph node | 11.8 | Ovarian ca. OVCAR- 8 | 9.3 |
| Colorectal | 10.4 | Ovarian ca. IGROV- 1 | 12.0 |
| Stomach | 7.8 | Ovarian ca.* (ascites) SK-OV-3 | 100.0 |

| | | | |
|--------------------------------|------|----------|-----|
| colon ca.* SW620(SW480 met) | 42.9 | Prostate | 5.7 |
|--------------------------------|------|----------|-----|

| | | | |
|----------------------------------|------|------------------------------|------|
| Colon ca. HT29 | 9.9 | Prostate ca.* (bone met)PC-3 | 78.5 |
| Colon ca. HCT-116 | 26.2 | Testis | 9.7 |
| Colon ca. CaCo-2 | 41.5 | Melanoma Hs688(A).T | 5.9 |
| Colon ca. tissue(ODO3866) | 6.3 | Melanoma* (met) Hs688(B).T | 14.2 |
| Colon ca. HCC-2998 | 16.0 | Melanoma UACC-62 | 14.0 |
| Gastric ca.* (liver met) NCI-N87 | 18.8 | Melanoma M14 | 5.7 |
| Bladder | 30.6 | Melanoma LOX IMVI | 8.8 |
| Trachea | 3.2 | Melanoma* (met) SK-MEL-5 | 14.7 |
| Kidney | 9.6 | Adipose | 18.9 |

Table MH. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3023, Run 164516146 | Rel. Exp.(%) Ag3373, Run 165296617 | Tissue Name | Rel. Exp.(%) Ag3023, Run 164516146 | Rel. Exp.(%) Ag3373, Run 165296617 |
|--------------------|---|---|---|---|---|
| Secondary Th1 act | 18.6 | 17.9 | HUVEC IL-1beta | 20.3 | 18.6 |
| Secondary Th2 act | 24.3 | 28.5 | HUVEC IFN gamma | 25.3 | 22.7 |
| Secondary Tr1 act | 22.8 | 21.8 | HUVEC TNF alpha + IFN gamma | 16.3 | 18.0 |
| Secondary Th1 rest | 7.5 | 6.8 | HUVEC TNF alpha + IL4 | 18.2 | 13.4 |
| Secondary Th2 rest | 11.6 | 9.5 | HUVEC IL-11 | 13.7 | 9.9 |
| Secondary Tr1 rest | 12.1 | 10.7 | Lung Microvascular EC none | 25.7 | 21.6 |
| Primary Th1 act | 20.7 | 16.5 | Lung Microvascular EC TNFalp + IL-1beta | 26.2 | 18.3 |
| Primary Th2 act | 20.2 | 19.3 | Microvascular Dermal EC none | 27.5 | 21.3 |

| | | | | | |
|------------------|------|------|-----------|------|------|
| Primary Th1 rest | 51.1 | 51.4 | Bronchial | 13.0 | 16.3 |
|------------------|------|------|-----------|------|------|

| | | | | | |
|---------------------------------------|------|------|---|------|------|
| | | | epithelium TNFalpha + IL1beta | | |
| Primary Th2 rest | 26.2 | 29.5 | Small airway epithelium none | 8.1 | 8.5 |
| Primary Tr1 rest | 23.7 | 26.1 | Small airway epithelium TNFalpha + IL- 1beta | 50.3 | 39.8 |
| CD45RA CD4 lymphocyte act | 14.6 | 11.0 | Coronery artery SMC rest | 20.2 | 18.9 |
| CD45RO CD4 lymphocyte act | 25.2 | 22.4 | Coronery artery SMC TNFalpha + IL-1beta | 12.0 | 9.8 |
| CD8 lymphocyte act | 20.4 | 15.8 | Astrocytes rest | 10.4 | 11.1 |
| Secondary CD8 lymphocyte rest | 16.5 | 19.9 | Astrocytes TNFalpha + IL- 1beta | 11.7 | 9.8 |
| Secondary CD8 lymphocyte act | 13.2 | 9.3 | KU-812 (Basophil) rest | 47.6 | 38.2 |
| CD4 lymphocyte none | 17.1 | 11.6 | KU-812 (Basophil) PMA/ionomycin | 94.0 | 92.0 |
| 2ry Th1/Th2/Tr1_anti- CD95 CH11 | 18.3 | 16.6 | CCD1106 (Keratinocytes) none | 19.9 | 13.2 |
| LAK cells rest | 25.5 | 16.0 | CCD1106 (Keratinocytes) TNFalpha + IL- 1beta | 6.0 | 4.8 |
| LAK cells IL-2 | 27.2 | 22.5 | Liver cirrhosis | 3.1 | 2.7 |
| LAK cells IL-2+IL- 12 | 27.2 | 19.3 | Lupus kidney | 2.1 | 1.7 |
| LAK cells IL- 2+IFN gamma | 36.3 | 34.4 | NCI-H292 none | 30.1 | 18.9 |
| LAK cells IL-2+ IL-18 | 35.1 | 29.7 | NCI-H292 IL-4 | 33.9 | 34.6 |
| LAK cells PMA/ionomycin | 12.4 | 11.0 | NCI-H292 IL-9 | 40.1 | 29.1 |
| NK Cells IL-2 rest | 20.0 | 15.0 | NCI-H292 IL-13 | 16.2 | 14.2 |
| Two Way MLR 3 | ~1.0 | ~1.7 | NCI-H292 IFN | ~1.6 | ~1.4 |

| | | | | | |
|---------------|------|-----|-----------|------|------|
| Two Way MLR 7 | 11.4 | 9.5 | HPAEC INF | 25.3 | 25.3 |
|---------------|------|-----|-----------|------|------|

| day | | | alpha + IL-1 beta | | . |
|---------------------------------|-------|-------|---|------|------|
| PBMC rest | 13.7 | 10.5 | Lung fibroblast none | 11.4 | 14.2 |
| PBMC PWM | 69.3 | 66.4 | Lung fibroblast TNF alpha + IL-1 beta | 6.1 | 7.2 |
| PBMC PHA-L | 22.8 | 17.7 | Lung fibroblast IL-4 | 28.5 | 29.1 |
| Ramos (B cell) none | 24.1 | 19.3 | Lung fibroblast IL-9 | 23.0 | 23.3 |
| Ramos (B cell) ionomycin | 100.0 | 100.0 | Lung fibroblast IL-13 | 20.6 | 18.9 |
| B lymphocytes PWM | 71.7 | 74.2 | Lung fibroblast IFN gamma | 39.0 | 32.5 |
| B lymphocytes CD40L and IL-4 | 29.1 | 28.7 | Dermal fibroblast CCD1070 rest | 33.9 | 31.0 |
| EOL-1 dbcAMP | 12.1 | 10.5 | Dermal fibroblast CCD1070 TNF alpha | 76.8 | 62.0 |
| EOL-1 dbcAMP PMA/ionomycin | 14.5 | 10.9 | Dermal fibroblast CCD1070 IL-1 beta | 20.3 | 13.9 |
| Dendritic cells none | 13.2 | 14.8 | Dermal fibroblast IFN gamma | 14.2 | 9.5 |
| Dendritic cells LPS | 11.7 | 8.3 | Dermal fibroblast IL-4 | 26.4 | 20.4 |
| Dendritic cells anti- CD40 | 17.7 | 12.7 | IBD Colitis 2 | 2.6 | 2.2 |
| Monocytes rest | 16.7 | 17.6 | IBD Crohn's | 2.0 | 1.9 |
| Monocytes LPS | 6.4 | 5.0 | Colon | 11.9 | 10.5 |
| Macrophages rest | 23.5 | 22.8 | Lung | 13.3 | 11.2 |
| Macrophages LPS | 9.9 | 7.1 | Thymus | 14.4 | 12.9 |
| HUVEC none | 20.6 | 17.9 | Kidney | 27.5 | 19.6 |
| HUVEC starved | 43.5 | 38.4 | | | |

CNS_neurodegeneration_v1.0 Summary: Ag3023/Ag3373 This panel does not show differential expression of the CG56804-03 gene, a splice variant of CG56804-01, in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

CG56804-03 has been assigned to the splice variant CG58564-03. Expression of this

General_screening_panel_v1.4 Summary: Ag3373 Highest expression of the CG56804-03 gene is seen in a prostate cancer cell line (CT=27). Overall, this gene is expressed at moderate levels in the cancer cell lines in this panel. A higher level of expression is observed in clusters of cell lines derived from prostate, brain, melanoma, colon, lung, breast and ovarian cancer when compared to expression in normal prostate, brain, colon, lung, breast and ovary. Thus, this gene could potentially be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, this gene product has moderate levels of expression in adipose, heart, skeletal muscle, adrenal, pituitary, thyroid and pancreas. Thus, this gene product may be a small molecule target for the treatment of endocrine and metabolic diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene appears to be differentially expressed in fetal (CT value = 29) vs adult liver (CT value =33) and may be useful for differentiation between the two sources of this tissue.

This gene is also expressed at moderate levels in all central nervous system samples present on this panel. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.5 Summary: Ag5847 - This primer pair, specific to this splice variant, CG58564-03. Expression of this variant is highest in salivary gland (CT=28.6). Therefore, expression of this gene can be used to differentiate this sample from others on the panel.

Panel 1.3D Summary: Ag3023 The CG56804-03 gene is ubiquitously expressed among the samples on this panel, with highest expression in an ovarian cancer cell line (CT=28.8). Overall, the expression of this gene shows good agreement with panel 1.4. A higher level of expression is observed in prostate, brain, melanoma, colon, lung, pancreatic, breast and ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and

ovary. Inhibition of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, expression of this gene is widespread, as in the previous panel. Please see Panel 1.4 for discussion of utility of this gene in metabolic disease.

This gene represents a dual specificity phosphatase that is also expressed at low to moderate levels across the CNS. Dual-specificity phosphatases comprise a family of MAP kinase regulating enzymes, members of which are upregulated in brains subjected to insults such as ischemia and seizure activity. MAP kinases are known to regulate neurotrophic and neurotoxic pathways. Consequently, agents that modulate the activity of this gene may have utility in attenuating the apoptotic and neurodegenerative processes following brain insults.

Panel 4.1D Summary: Ag5847 - This primer pair recognizes a splice variant of CG58564-03. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3023/Ag3373 The CG56804-03 gene is expressed at high to moderate levels in a wide range of cell types and tissues of significance in the immune response in health and disease. Highest expression of this gene is seen in ionomycin treated Ramos B cells (CT=26.83). Therefore, targeting of this gene product with a small molecule drug or antibody therapeutic may modulate the functions of cells of the immune system as well as resident tissue cells and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, and arthritis, including osteoarthritis and rheumatoid arthritis.

N. CG58564-04: Dual specificity phosphatase

Expression of gene CG58564-04, a splice variant of CG58564-01, was assessed using the primer-probe sets Ag3023, Ag3373 and Ag5844, described in Tables NA, NB and NC. Results of the RTQ-PCR runs are shown in Tables ND, NE, NF and NG.

Table NA. Probe Name Ag3023

| Primers | Sequences | Length | 5' to 3' Position | Access No: |
|---------|------------------------------|--------|-------------------|------------|
| Forward | 5'-ctaatgctggatttgtccatca-3' | 22 | 190 | 417 |

| | | | | |
|---------|---|----|-----|-----|
| Probe | TET-5'-tcaggaatatgaagccatctacacctaga-3'-TAMRA | 28 | 159 | 418 |
| Reverse | 5'-tggagtggtgacatcatctgta-3' | 22 | 127 | 419 |

Table NB. Probe Name Ag3373

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-atttgtccatcaacttcaggaa-3' | 22 | 180 | 420 |
| Probe | TET-5'-tgaagccatctacacctagaaaattaaca-3'-TAMRA | 28 | 150 | 421 |
| Reverse | 5'-tggagtggtgacatcatctgta-3' | 22 | 127 | 422 |

Table NC. Probe Name Ag5844

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-ccttagtctaaataactgctg-3' | 21 | 377 | 423 |
| Probe | TET-5'-agtttgttcaatattttgtcgatgcata-3'-TAMRA | 30 | 415 | 424 |
| Reverse | 5'-aggagtggacctaccctat-3' | 19 | 552 | 425 |

Table ND. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3023, Run 209821074 | Rel. Exp.(%) Ag3373, Run 210154071 | Tissue Name | Rel. Exp.(%) Ag3023, Run 209821074 | Rel. Exp.(%) Ag3373, Run 210154071 |
|-------------|--|--|-------------------------------|--|--|
| AD 1 Hippo | 10.9 | 16.8 | Control (Path) 3 Temporal Ctx | 9.1 | 8.0 |
| AD 2 Hippo | 34.2 | 37.6 | Control (Path) 4 Temporal Ctx | 40.6 | 65.5 |
| AD 3 Hippo | 12.0 | 15.8 | AD 1 Occipital Ctx | 24.7 | 29.1 |
| AD 4 Hippo | 13.8 | 10.3 | AD 2 Occipital Ctx (Missing) | 0.0 | 0.0 |

| | | | | | |
|------------|------|------|------|------|------|
| AD 6 Hippo | 80.7 | 72.2 | AD 4 | 35.4 | 22.4 |
|------------|------|------|------|------|------|

| | | | | | |
|----------------------------|--------------|--------------|---|------|------|
| | | | Occipital Ctx | | |
| Control 2 Hippo | 35.8 | 38.4 | AD 5 Occipital Ctx | 3.9 | 30.4 |
| Control 4 Hippo | 16.5 | 11.7 | AD 6 Occipital Ctx | 46.0 | 37.4 |
| Control (Path) 3 Hippo | 13.1 | 15.4 | Control 1 Occipital Ctx | 9.9 | 10.7 |
| AD 1 Temporal Ctx | 39.0 | 31.4 | Control 2 Occipital Ctx | 39.0 | 38.4 |
| AD 2 Temporal Ctx | 38.7 | 73.2 | Control 3 Occipital Ctx | 23.0 | 20.6 |
| AD 3 Temporal Ctx | 9.5 | 13.2 | Control 4 Occipital Ctx | 13.3 | 13.3 |
| AD 4 Temporal Ctx | 27.9 | 34.9 | Control (Path) 1 Occipital Ctx | 80.1 | 76.3 |
| AD 5 Inf Temporal Ctx | 59.0 | 100.0 | Control (Path) 2 Occipital Ctx | 17.3 | 20.0 |
| AD 5 SupTemporal Ctx | 33.2 | 44.1 | Control (Path) 3 Occipital Ctx | 8.4 | 8.7 |
| AD 6 Inf Temporal Ctx | 100.0 | 73.2 | Control (Path) 4 Occipital Ctx | 21.2 | 20.6 |
| AD 6 Sup Temporal Ctx | 79.6 | 80.1 | Control 1 Parietal Ctx | 12.1 | 16.3 |
| Control 1 Temporal Ctx | 10.2 | 13.7 | Control 2 Parietal Ctx | 48.0 | 40.9 |
| Control 2 Temporal Ctx | 41.2 | 31.9 | Control 3 Parietal Ctx | 17.9 | 16.3 |
| | | | Control | | |

| Control 4 Temporal Ctx | 9.5 | 38.4 | Control (Path) 2 | 23.0 | 30.4 |
|---------------------------|-----|------|---------------------|------|------|
| | | | | | |

| | | | | | |
|----------------------------------|------|------|-------------------------------------|------|------|
| | | | Parietal Ctx | | |
| Control (Path) 1 Temporal Ctx | 59.9 | 68.3 | Control (Path) 3 Parietal Ctx | 10.2 | 9.0 |
| Control (Path) 2 Temporal Ctx | 40.3 | 41.2 | Control (Path) 4 Parietal Ctx | 44.8 | 43.8 |

Table NE. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3373, Run 217043119 | Tissue Name | Rel. Exp.(%) Ag3373, Run 217043119 |
|-------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 12.0 | Renal ca. TK-10 | 20.3 |
| Melanoma* Hs688(A).T | 30.8 | Bladder | 23.2 |
| Melanoma* Hs688(B).T | 69.3 | Gastric ca. (liver met.) NCI-N87 | 25.3 |
| Melanoma* M14 | 15.0 | Gastric ca. KATO III | 30.8 |
| Melanoma* LOXIMVI | 26.6 | Colon ca. SW-948 | 9.7 |
| Melanoma* SK-MEL-5 | 21.5 | Colon ca. SW480 | 35.1 |
| Squamous cell carcinoma SCC-4 | 33.0 | Colon ca.* (SW480 met) SW620 | 13.9 |
| Testis Pool | 19.8 | Colon ca. HT29 | 8.5 |
| Prostate ca.* (bone met) PC-3 | 100.0 | Colon ca. HCT-116 | 36.9 |
| Prostate Pool | 9.2 | Colon ca. CaCo-2 | 42.9 |
| Placenta | 3.8 | Colon cancer tissue | 9.0 |
| Uterus Pool | 7.4 | Colon ca. SW1116 | 5.8 |
| Ovarian ca. OVCAR-3 | 28.5 | Colon ca. Colo-205 | 4.3 |
| Ovarian ca. SK-OV-3 | 40.3 | Colon ca. SW-48 | 4.2 |
| Ovarian ca. OVCAR-4 | 20.0 | Colon Pool | 20.7 |
| Ovarian ca. OVCAR-5 | 35.1 | Small Intestine Pool | 12.2 |
| Ovarian ca. IGROV-1 | 10.9 | Stomach Pool | 9.9 |

| | | | |
|-----------------|------|-----------------|------|
| Breast ca. MCF | 37.6 | Heart Pool | 11.6 |
| Breast ca. MDA- | 37.1 | Lymph Node Pool | 17.9 |

| | | | |
|-------------------|------|-------------------------------------|------|
| MB-231 | | | |
| Breast ca. BT 549 | 62.4 | Fetal Skeletal Muscle | 12.3 |
| Breast ca. T47D | 61.1 | Skeletal Muscle Pool | 16.0 |
| Breast ca. MDA-N | 10.0 | Spleen Pool | 11.6 |
| Breast Pool | 17.3 | Thymus Pool | 12.2 |
| Trachea | 12.0 | CNS cancer (glio/astro) U87-MG | 29.1 |
| Lung | 6.7 | CNS cancer (glio/astro) U-118-MG | 69.3 |
| Fetal Lung | 34.2 | CNS cancer (neuro;met) SK-N-AS | 34.9 |
| Lung ca. NCI-N417 | 5.4 | CNS cancer (astro) SF-539 | 19.1 |
| Lung ca. LX-1 | 17.2 | CNS cancer (astro) SNB-75 | 35.8 |
| Lung ca. NCI-H146 | 3.0 | CNS cancer (glio) SNB-19 | 11.3 |
| Lung ca. SHP-77 | 18.6 | CNS cancer (glio) SF-295 | 26.4 |
| Lung ca. A549 | 29.1 | Brain (Amygdala) Pool | 4.5 |
| Lung ca. NCI-H526 | 4.6 | Brain (cerebellum) | 8.1 |
| Lung ca. NCI-H23 | 31.6 | Brain (fetal) | 13.2 |
| Lung ca. NCI-H460 | 18.2 | Brain (Hippocampus) Pool | 5.3 |
| Lung ca. HOP-62 | 14.1 | Cerebral Cortex Pool | 5.4 |
| Lung ca. NCI-H522 | 31.6 | Brain (Substantia nigra) Pool | 4.8 |
| Liver | 1.2 | Brain (Thalamus) Pool | 8.0 |
| Fetal Liver | 32.3 | Brain (whole) | 6.2 |
| Liver ca. HepG2 | 14.6 | Spinal Cord Pool | 6.6 |
| Kidney Pool | 22.1 | Adrenal Gland | 8.1 |
| Fetal Kidney | 26.1 | Pituitary gland Pool | 3.0 |
| Renal ca. 786-0 | 28.7 | Salivary Gland | 4.7 |
| Renal ca. A498 | 11.3 | Thyroid (female) | 4.4 |
| Renal ca. ACHN | 12.2 | Pancreatic ca. CAPAN2 | 17.3 |
| Renal ca. UO-31 | 24.1 | Pancreas Pool | 17.1 |

Table NF. Panel 1.3D

| Rel. Exp. (%) Ag3023 | | Rel. Exp. (%) Ag3023 | |
|----------------------|-----|----------------------|------|
| Pancreas | 0.1 | Renal ca. 786-0 | 34.2 |

| | | | |
|--------------------------|------|-----------------------------------|------|
| Pancreatic ca. CAPAN 2 | 17.7 | Renal ca. A498 | 17.6 |
| Adrenal gland | 3.8 | Renal ca. RXF 393 | 17.2 |
| Thyroid | 3.0 | Renal ca. ACHN | 13.5 |
| Salivary gland | 3.9 | Renal ca. UO-31 | 0.0 |
| Pituitary gland | 3.6 | Renal ca. TK-10 | 23.0 |
| Brain (fetal) | 8.1 | Liver | 11.7 |
| Brain (whole) | 8.5 | Liver (fetal) | 8.0 |
| Brain (amygdala) | 6.7 | Liver ca. (hepatoblast) HepG2 | 26.2 |
| Brain (cerebellum) | 15.2 | Lung | 3.1 |
| Brain (hippocampus) | 5.4 | Lung (fetal) | 11.0 |
| Brain (substantia nigra) | 9.0 | Lung ca. (small cell) LX-1 | 12.9 |
| Brain (thalamus) | 4.2 | Lung ca. (small cell) NCI-H69 | 9.9 |
| Cerebral Cortex | 2.0 | Lung ca. (s.cell var.) SHP-77 | 67.8 |
| Spinal cord | 6.9 | Lung ca. (large cell)NCI-H460 | 3.4 |
| Glio/astro U87-MG | 28.5 | Lung ca. (non-sm. cell) A549 | 45.1 |
| Glio/astro U-118-MG | 46.7 | Lung ca. (non-s.cell) NCI-H23 | 22.7 |
| astrocytoma SW1783 | 40.6 | Lung ca. (non-s.cell) HOP-62 | 25.7 |
| neuro*; met SK-N-AS | 27.2 | Lung ca. (non-s.cl) NCI-H522 | 38.2 |
| astrocytoma SF-539 | 29.7 | Lung ca. (squam.) SW 900 | 27.4 |
| astrocytoma SNB-75 | 35.1 | Lung ca. (squam.) NCI-H596 | 29.9 |
| glioma SNB-19 | 15.6 | Mammary gland | 5.1 |
| glioma U251 | 37.9 | Breast ca.* (pl.ef) MCF-7 | 47.0 |
| glioma SF-295 | 18.4 | Breast ca.* (pl.ef) MDA-MB-231 | 22.7 |
| Heart (fetal) | 2.9 | Breast ca.* (pl.ef) T47D | 86.5 |
| Heart | 12.9 | Breast ca. BT-549 | 15.9 |

Bone marrow

| | | | |
|-------------------------------------|------|-----------------------------------|--------------|
| Thymus | 14.3 | Ovarian ca. OVCAR-4 | 16.3 |
| Spleen | 8.7 | Ovarian ca. OVCAR-5 | 83.5 |
| Lymph node | 11.8 | Ovarian ca. OVCAR-8 | 9.3 |
| Colorectal | 10.4 | Ovarian ca. IGROV-1 | 12.0 |
| Stomach | 7.8 | Ovarian ca.* (ascites) SK-OV-3 | 100.0 |
| Small intestine | 5.1 | Uterus | 4.9 |
| Colon ca. SW480 | 19.3 | Placenta | 1.3 |
| Colon ca.* SW620(SW480 met) | 42.9 | Prostate | 3.9 |
| Colon ca. HT29 | 9.9 | Prostate ca.* (bone met)PC-3 | 78.5 |
| Colon ca. HCT-116 | 26.2 | Testis | 9.7 |
| Colon ca. CaCo-2 | 41.5 | Melanoma Hs688(A).T | 5.9 |
| Colon ca. tissue(ODO3866) | 6.3 | Melanoma* (met) Hs688(B).T | 14.2 |
| Colon ca. HCC-2998 | 16.0 | Melanoma UACC-62 | 14.0 |
| Gastric ca.* (liver met) NCI-N87 | 18.8 | Melanoma M14 | 5.7 |
| Bladder | 30.6 | Melanoma LOX IMVI | 8.8 |
| Trachea | 3.2 | Melanoma* (met) SK-MEL-5 | 14.7 |
| Kidney | 9.6 | Adipose | 18.9 |

Table NG. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3023, Run 164516146 | Rel. Exp.(%) Ag3373, Run 165296617 | Tissue Name | Rel. Exp.(%) Ag3023, Run 164516146 | Rel. Exp.(%) Ag3373, Run 165296617 |
|-------------------|---|---|--------------------|---|---|
| Secondary Th1 act | 18.6 | 17.9 | HUVEC IL-1beta | 20.3 | 18.6 |
| Secondary Th2 act | 24.3 | 28.5 | HUVEC IFN gamma | 25.3 | 22.7 |
| | | | HUVEC TNF | | |

| | | | |
|-------------------|------|------|-------------|
| Secondary Th1 act | 18.6 | 17.9 | HUVEC TNF |
| | | | alpha + IL4 |

| | | | | | |
|---------------------------------------|------|------|---|------|------|
| Secondary Th2 rest | 11.6 | 9.5 | HUVEC IL-11 | 13.7 | 9.9 |
| Secondary Tr1 rest | 12.1 | 10.7 | Lung Microvascular EC none | 25.7 | 21.6 |
| Primary Th1 act | 20.7 | 16.5 | Lung Microvascular EC TNFalpha + IL-1beta | 26.2 | 18.3 |
| Primary Th2 act | 20.2 | 19.3 | Microvascular Dermal EC none | 27.5 | 21.3 |
| Primary Tr1 act | 23.3 | 27.7 | Microvasular Dermal EC TNFalpha + IL-1beta | 20.7 | 19.9 |
| Primary Th1 rest | 51.1 | 51.4 | Bronchial epithelium TNFalpha + IL1beta | 13.0 | 16.3 |
| Primary Th2 rest | 26.2 | 29.5 | Small airway epithelium none | 8.1 | 8.5 |
| Primary Tr1 rest | 23.7 | 26.1 | Small airway epithelium TNFalpha + IL-1beta | 50.3 | 39.8 |
| CD45RA CD4 lymphocyte act | 14.6 | 11.0 | Coronery artery SMC rest | 20.2 | 18.9 |
| CD45RO CD4 lymphocyte act | 25.2 | 22.4 | Coronery artery SMC TNFalpha + IL-1beta | 12.0 | 9.8 |
| CD8 lymphocyte act | 20.4 | 15.8 | Astrocytes rest | 10.4 | 11.1 |
| Secondary CD8 lymphocyte rest | 16.5 | 19.9 | Astrocytes TNFalpha + IL-1beta | 11.7 | 9.8 |
| Secondary CD8 lymphocyte act | 13.2 | 9.3 | KU-812 (Basophil) rest | 47.6 | 38.2 |
| CD4 lymphocyte none | 17.1 | 11.6 | KU-812 (Basophil) PMA/ionomycin | 94.0 | 92.0 |
| 2ry Th1/Th2/Tr1_anti- CD95 CH11 | 18.3 | 16.6 | CCD1106 (Keratinocytes) none | 19.9 | 13.2 |

CCD1106

| | | | Delta | | |
|------------------|------|------|-----------------|-----|-----|
| I-LAK cells IL-2 | 27.2 | 22.5 | Liver cirrhosis | 3.1 | 2.7 |

| | | | | | |
|------------------------------|--------------|--------------|---------------------------------------|------|------|
| LAK cells IL-2+IL-12 | 27.2 | 19.3 | Lupus kidney | 2.1 | 1.7 |
| LAK cells IL-2+IFN gamma | 36.3 | 34.4 | NCI-H292 none | 30.1 | 18.9 |
| LAK cells IL-2+IL-18 | 35.1 | 29.7 | NCI-H292 IL-4 | 33.9 | 34.6 |
| LAK cells PMA/ionomycin | 12.4 | 11.0 | NCI-H292 IL-9 | 40.1 | 29.1 |
| NK Cells IL-2 rest | 20.0 | 15.0 | NCI-H292 IL-13 | 16.2 | 14.2 |
| Two Way MLR 3 day | 24.0 | 16.7 | NCI-H292 IFN gamma | 16.6 | 18.4 |
| Two Way MLR 5 day | 12.9 | 10.1 | HPAEC none | 13.6 | 13.5 |
| Two Way MLR 7 day | 11.4 | 9.5 | HPAEC TNF alpha + IL-1 beta | 25.3 | 25.3 |
| PBMC rest | 13.7 | 10.5 | Lung fibroblast none | 11.4 | 14.2 |
| PBMC PWM | 69.3 | 66.4 | Lung fibroblast TNF alpha + IL-1 beta | 6.1 | 7.2 |
| PBMC PHA-L | 22.8 | 17.7 | Lung fibroblast IL-4 | 28.5 | 29.1 |
| Ramos (B cell) none | 24.1 | 19.3 | Lung fibroblast IL-9 | 23.0 | 23.3 |
| Ramos (B cell) ionomycin | 100.0 | 100.0 | Lung fibroblast IL-13 | 20.6 | 18.9 |
| B lymphocytes PWM | 71.7 | 74.2 | Lung fibroblast IFN gamma | 39.0 | 32.5 |
| B lymphocytes CD40L and IL-4 | 29.1 | 28.7 | Dermal fibroblast CCD1070 rest | 33.9 | 31.0 |
| EOL-1 dbcAMP | 12.1 | 10.5 | Dermal fibroblast CCD1070 TNF alpha | 76.8 | 62.0 |
| EOL-1 dbcAMP PMA/ionomycin | 14.5 | 10.9 | Dermal fibroblast CCD1070 IL-1 beta | 20.3 | 13.9 |
| Dendritic cells none | 13.2 | 14.8 | Dermal fibroblast IFN gamma | 14.2 | 9.5 |
| Dendritic cells LPS | 11.7 | 8.3 | Dermal fibroblast IL-4 | 26.4 | 20.4 |
| Dendritic cells anti-CD40 | 17.7 | 12.7 | IBD Colitis 2 | 2.6 | 2.2 |

| | | | | | |
|------------------|------|------|------|------|------|
| Macrophages rest | 24.8 | 22.8 | Lung | 13.8 | 11.2 |
|------------------|------|------|------|------|------|

| | | | | | |
|-----------------|------|------|--------|------|------|
| Macrophages LPS | 9.9 | 7.1 | Thymus | 14.4 | 12.9 |
| HUVEC none | 20.6 | 17.9 | Kidney | 27.5 | 19.6 |
| HUVEC starved | 43.5 | 38.4 | | | |

CNS_neurodegeneration_v1.0 Summary: Ag3023/Ag3373 This panel does not show differential expression of the CG56804-04 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system. Ag5847 - This primer pair recognizes a splice variant of CG58564-01 designated CG58564-04. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3373 Highest expression of the CG56804-04 gene is seen in a prostate cancer cell line (CT=27). Overall, this gene is expressed at moderate levels in the cancer cell lines in this panel. A higher level of expression is observed in clusters of cell lines derived from prostate, brain, melanoma, colon, lung, breast and ovarian cancer when compared to expression in normal prostate, brain, colon, lung, breast and ovary. Thus, this gene could potentially be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, this gene product has moderate levels of expression in adipose, heart, skeletal muscle, adrenal, pituitary, thyroid and pancreas. Thus, this gene product may be a small molecule target for the treatment of endocrine and metabolic diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene appears to be differentially expressed in fetal (CT value = 29) vs adult liver (CT value = 33) and may be useful for differentiation between the two sources of this tissue.

This gene is also expressed at moderate levels in all central nervous system samples present on this panel. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

For more information on this panel, please see WO 02/072757.

All samples on this panel (data not shown).

Panel 1.3D Summary: Ag3023 The CG56804-04 gene is ubiquitously expressed among the samples on this panel, with highest expression in an ovarian cancer cell line (CT=28.8). Overall, the expression of this gene shows good agreement with panel 1.4. A higher level of expression is observed in prostate, brain, melanoma, colon, lung, pancreatic, breast and ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and ovary. Thus, expression of this gene could be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, expression of this gene is widespread, as in the previous panel. Please see Panel 1.4 for discussion of utility of this gene in metabolic disease.

This gene represents a dual specificity phosphatase that is also expressed at low to moderate levels across the CNS. Dual-specificity phosphatases comprise a family of MAP kinase regulating enzymes, members of which are upregulated in brains subjected to insults such as ischemia and seizure activity. MAP kinases are known to regulate neurotrophic and neurotoxic pathways. Consequently, agents that modulate the activity of this gene may have utility in attenuating the apoptotic and neurodegenerative processes following brain insults.

Panel 4.1D Summary: Ag5844 - This primer pair recognizes a splice variant of CG58564-01. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3023/Ag3373 The CG56804-04 gene is expressed at high to moderate levels in a wide range of cell types and tissues of significance in the immune response in health and disease. Highest expression of this gene is seen in ionomycin treated Ramos B cells (CT=26.83). Therefore, targeting of this gene product with a small molecule drug or antibody therapeutic may modulate the functions of cells of the immune system as well as resident tissue cells and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, and arthritis, including osteoarthritis and rheumatoid arthritis.

3. CG56810-01 RPPC-D INTERACTING PROTEIN 1

described in Table OA. Results of the RTQ-PCR runs are shown in Tables OB and OC.

Table OA. Probe Name Ag3338

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -cccattcagcactgaaacag-3' | 20 | 3021 | 426 |
| Probe | TET-5' -tcctgtaaatgacaaagaatccctctgaaca-3' - TAMRA | 30 | 3055 | 427 |
| Reverse | 5' -tgcttcaactgacttcagaacct-3' | 22 | 3085 | 428 |

Table OB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3338, Run 215773746 | Tissue Name | Rel. Exp.(%) Ag3338, Run 215773746 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 1.1 | Renal ca. TK-10 | 0.8 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 1.1 |
| Melanoma* Hs688(B).T | 0.0 | Gastric ca. (liver mct.) NCI-N87 | 0.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 0.0 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |
| Melanoma* SK- MEL-5 | 0.2 | Colon ca. SW480 | 0.4 |
| Squamous cell carcinoma SCC-4 | 0.0 | Colon ca.* (SW480 met) SW620 | 0.0 |
| Testis Pool | 100.0 | Colon ca. HT29 | 0.5 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 0.2 |
| Prostate Pool | 1.0 | Colon ca. CaCo-2 | 1.0 |
| Placenta | 0.0 | Colon cancer tissue | 0.9 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.2 |
| Ovarian ca. OVCAR-3 | 0.9 | Colon ca. Colo-205 | 0.2 |
| Ovarian ca. SK-OV- 3 | 0.0 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 1.2 | Colon Pool | 0.5 |
| Ovarian ca. OVCAR-5 | 3.5 | Small Intestine Pool | 0.3 |
| Ovarian ca. IGROV- 1 | 0.0 | Stomach Pool | 0.2 |

(a) b (b) c (c) d (d) e (e) f (f) g (g) h (h) i (i) j (j) k (k) l (l) m (m) n (n) o (o) p (p) q (q) r (r) s (s) t (t) u (u) v (v) w (w) x (x) y (y) z (z)

| | | | |
|-----------------------|-----|-------------------------------------|-----|
| Breast ca. MCF-7 | 1.9 | Heart Pool | 1.1 |
| Breast ca. MDA-MB-231 | 1.2 | Lymph Node Pool | 1.4 |
| Breast ca. BT 549 | 0.2 | Fetal Skeletal Muscle | 0.2 |
| Breast ca. T47D | 6.7 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 1.4 |
| Breast Pool | 0.5 | Thymus Pool | 0.0 |
| Trachea | 0.9 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 0.2 | CNS cancer (glio/astro) U-118-MG | 0.0 |
| Fetal Lung | 0.4 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 0.8 | CNS cancer (astro) SNB-75 | 0.0 |
| Lung ca. NCI-H146 | 0.5 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 0.1 | CNS cancer (glio) SF-295 | 0.2 |
| Lung ca. A549 | 1.5 | Brain (Amygdala) Pool | 0.7 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 0.6 |
| Lung ca. NCI-H23 | 1.5 | Brain (fetal) | 0.9 |
| Lung ca. NCI-H460 | 0.0 | Brain (Hippocampus) Pool | 0.7 |
| Lung ca. HOP-62 | 3.0 | Cerebral Cortex Pool | 0.2 |
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) Pool | 0.7 |
| Liver | 0.4 | Brain (Thalamus) Pool | 1.3 |
| Fetal Liver | 0.5 | Brain (whole) | 0.0 |
| Liver ca. HepG2 | 0.2 | Spinal Cord Pool | 0.9 |
| Kidney Pool | 0.9 | Adrenal Gland | 0.0 |
| Fetal Kidney | 0.6 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 0.0 |
| Renal ca. A498 | 0.0 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 3.4 |
| Renal ca. UO-31 | 0.0 | Pancreas Pool | 0.8 |

Table OC Panel 4D

| Tissue Name | Ag3338, Run 165221737 | Tissue Name | Ag3338, Run 165221737 |
|-------------|--------------------------|-------------|--------------------------|
|-------------|--------------------------|-------------|--------------------------|

| | | | |
|--------------------------------|-----|---|-----|
| Secondary Th1 act | 0.0 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 0.0 | HUVEC IFN gamma | 6.9 |
| Secondary Tr1 act | 0.0 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 2.6 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 1.9 |
| Primary Tr1 act | 0.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 0.0 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 0.0 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 0.0 | Coronery artery SMC rest | 0.0 |
| CD45RO CD4 lymphocyte act | 0.0 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 4.0 | Astrocytes rest | 0.0 |
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 0.0 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.0 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 0.0 |
| LAK cells rest | 4.6 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 0.0 |
| LAK cells IL-2+IL-12 | 0.0 | Lupus kidney | 2.4 |
| LAK cells IL-2+IFN gamma | 0.0 | NCI-H292 none | 0.0 |
| LAK cells IL-2+ IL-18 | 0.0 | NCI-H292 IL-4 | 4.5 |
| LAK cells | | | |

| | | | |
|-------------------|-----|--------------------|-----|
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 0.0 |
| Two Way MLR 5 day | 0.0 | HPAEC none | 0.0 |

| | | | |
|------------------------------|-------|---------------------------------------|------|
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 14.0 | Lung fibroblast none | 0.0 |
| PBMC PWM | 0.0 | Lung fibroblast TNF alpha + IL-1 beta | 0.0 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 3.0 | Lung fibroblast IL-9 | 0.0 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 0.0 |
| B lymphocytes PWM | 0.0 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 rest | 0.0 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 |
| EOL-1 dbcAMP PMA/ionomycin | 4.7 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 13.9 | Dermal fibroblast IL-4 | 0.0 |
| Dendritic cells anti-CD40 | 6.0 | IBD Colitis 2 | 0.0 |
| Monocytes rest | 100.0 | IBD Crohn's | 0.0 |
| Monocytes LPS | 0.0 | Colon | 15.2 |
| Macrophages rest | 1.3 | Lung | 4.0 |
| Macrophages LPS | 0.0 | Thymus | 0.0 |
| HUVEC none | 0.0 | Kidney | 3.1 |
| HUVEC starved | 0.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3338 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3338 - Expression of this gene is highest in testis (CT=29.4). Therefore, expression of this gene could be used to distinguish this sample from others on the panel.

There is also low expression in pancreatic cancer cell line CAPAN2, lung cancer cell line HOP-62, breast cancer cell line T47D, and ovarian cancer cell line OVCAR-5. Thus,

Panel 4D Summary: Ag3338 - Significant expression of this gene is seen only in resting monocytes (CT=32.3) Therefore, expression of this gene can be used to differentiate between this sample and others on this panel.

P. CG57789-01 and CG57789-02: RAS-LIKE PROTEIN RRP22-like

Expression of gene CG57789-01 and variant CG57789-02 was assessed using the primer-probe set Ag3333, described in Table PA. Results of the RTQ-PCR runs are shown in Tables PB, PC and PD.

Table PA. Probe Name Ag3333

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-tcgactttccacccatcaag-3' | 19 | 181 | 429 |
| Probe | TET-5'-cttccctgtcaatacgctccaggagt-3' - TAMRA | 26 | 203 | 430 |
| Reverse | 5'-aggatgttaggcgtggacact-3' | 20 | 258 | 431 |

Table PB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3333, Run 210146459 | Tissue Name | Rel. Exp.(%) Ag3333, Run 210146459 |
|---------------------------|---------------------------------------|----------------------------------|---------------------------------------|
| AD 1 Hippo | 22.2 | Control (Path) 3 Temporal Ctx | 7.5 |
| AD 2 Hippo | 18.8 | Control (Path) 4 Temporal Ctx | 21.6 |
| AD 3 Hippo | 17.9 | AD 1 Occipital Ctx | 29.7 |
| AD 4 Hippo | 8.7 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 Hippo | 100.0 | AD 3 Occipital Ctx | 15.8 |
| AD 6 Hippo | 42.9 | AD 4 Occipital Ctx | 24.7 |
| Control 2 Hippo | 25.9 | AD 5 Occipital Ctx | 90.1 |
| Control 4 Hippo | 12.1 | AD 6 Occipital Ctx | 16.3 |
| Control (Path) 3 Hippo | 13.4 | Control 1 Occipital Ctx | 4.2 |
| AD 1 Temporal Ctx | 21.3 | Control 2 Occipital Ctx | 74.7 |
| | | Control 3 Occipital | |

| | | | |
|-------------------|------|------------------|------|
| AD 4 Temporal Ctx | 15.8 | Control (Path) 1 | 47.3 |
|-------------------|------|------------------|------|

| | | | |
|----------------------------------|------|-----------------------------------|------|
| | | Occipital Ctx | |
| AD 5 Inf Temporal Ctx | 92.0 | Control (Path) 2 Occipital Ctx | 13.5 |
| AD 5 Sup Temporal Ctx | 43.2 | Control (Path) 3 Occipital Ctx | 4.1 |
| AD 6 Inf Temporal Ctx | 26.4 | Control (Path) 4 Occipital Ctx | 14.6 |
| AD 6 Sup Temporal Ctx | 31.6 | Control 1 Parietal Ctx | 7.6 |
| Control 1 Temporal Ctx | 5.8 | Control 2 Parietal Ctx | 39.2 |
| Control 2 Temporal Ctx | 51.8 | Control 3 Parietal Ctx | 21.9 |
| Control 3 Temporal Ctx | 14.5 | Control (Path) 1 Parietal Ctx | 56.3 |
| Control 3 Temporal Ctx | 8.1 | Control (Path) 2 Parietal Ctx | 20.2 |
| Control (Path) 1 Temporal Ctx | 39.2 | Control (Path) 3 Parietal Ctx | 6.2 |
| Control (Path) 2 Temporal Ctx | 40.9 | Control (Path) 4 Parietal Ctx | 24.5 |

Table PC. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3333, Run 216516940 | Tissue Name | Rel. Exp.(%) Ag3333, Run 216516940 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 4.4 | Renal ca. TK-10 | 40.1 |
| Melanoma* Hs688(A).T | 0.9 | Bladder | 5.0 |
| Melanoma* Hs688(B).T | 1.8 | Gastric ca. (liver met.) NCI-N87 | 4.5 |
| Melanoma* M14 | 2.7 | Gastric ca. KATO III | 20.0 |
| Melanoma* LOXIMVI | 0.3 | Colon ca. SW-948 | 0.0 |
| Melanoma* SK-MEL-5 | 0.9 | Colon ca. SW480 | 100.0 |
| Squamous cell carcinoma SCC-4 | 0.1 | Colon ca.* (SW480 met) SW620 | 33.0 |
| Testis Pool | 2.1 | Colon ca. HT29 | 5.0 |
| Prostate ca.* (bone met) PC-3 | 2.4 | Colon ca. HCT-116 | 0.1 |

| | | | |
|-------------|------|--------------------|------|
| Cervix Pool | 0.5 | Colon ca. SW1116 | 16.2 |
| Ovarian ca. | 52.9 | Colon ca. Colo-205 | 0.2 |

| | | | |
|-----------------------|------|-------------------------------------|------|
| OVCAR-3 | | | |
| Ovarian ca. SK-OV-3 | 0.6 | Colon ca. SW-48 | 0.2 |
| Ovarian ca. OVCAR-4 | 17.9 | Colon Pool | 2.2 |
| Ovarian ca. OVCAR-5 | 4.5 | Small Intestine Pool | 1.0 |
| Ovarian ca. IGROV-1 | 0.9 | Stomach Pool | 0.9 |
| Ovarian ca. OVCAR-8 | 15.4 | Bone Marrow Pool | 1.8 |
| Ovary | 4.2 | Fetal Heart | 10.9 |
| Breast ca. MCF-7 | 0.7 | Heart Pool | 2.8 |
| Breast ca. MDA-MB-231 | 0.4 | Lymph Node Pool | 4.4 |
| Breast ca. BT 549 | 42.0 | Fetal Skeletal Muscle | 1.1 |
| Breast ca. T47D | 13.0 | Skeletal Muscle Pool | 46.7 |
| Breast ca. MDA-N | 0.1 | Spleen Pool | 0.0 |
| Breast Pool | 2.4 | Thymus Pool | 2.3 |
| Trachea | 2.4 | CNS cancer (glio/astro) U87-MG | 0.9 |
| Lung | 0.2 | CNS cancer (glio/astro) U-118-MG | 0.3 |
| Fetal Lung | 0.9 | CNS cancer (neuro;met) SK-N-AS | 69.7 |
| Lung ca. NCI-N417 | 17.1 | CNS cancer (astro) SF-539 | 2.2 |
| Lung ca. LX-1 | 1.1 | CNS cancer (astro) SNB-75 | 15.9 |
| Lung ca. NCI-H146 | 14.5 | CNS cancer (glio) SNB-19 | 0.6 |
| Lung ca. SHP-77 | 37.6 | CNS cancer (glio) SF-295 | 6.0 |
| Lung ca. A549 | 0.4 | Brain (Amygdala) Pool | 28.5 |
| Lung ca. NCI-H526 | 23.5 | Brain (cerebellum) | 29.1 |
| Lung ca. NCI-H23 | 8.2 | Brain (fetal) | 21.3 |
| Lung ca. NCI-H460 | 14.3 | Brain (Hippocampus) Pool | 27.7 |
| Lung ca. HOP-62 | 1.7 | Cerebral Cortex Pool | 36.1 |
| Lung ca. NCI-H522 | 86.5 | Brain (Substantia nigra) | 40.1 |

| Fetal Liver | | Brain (whole) | |
|-----------------|-----|------------------|------|
| Liver ca. HepG2 | 6.2 | Spinal Cord Pool | 12.3 |

| | | | |
|-----------------|------|-----------------------|------|
| Kidney Pool | 3.8 | Adrenal Gland | 4.7 |
| Fetal Kidney | 7.4 | Pituitary gland Pool | 3.7 |
| Renal ca. 786-0 | 0.2 | Salivary Gland | 48.0 |
| Renal ca. A498 | 20.9 | Thyroid (female) | 1.1 |
| Renal ca. ACHN | 8.5 | Pancreatic ca. CAPAN2 | 0.0 |
| Renal ca. UO-31 | 3.0 | Pancreas Pool | 4.0 |

Table PD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3333, Run 165084139 | Tissue Name | Rel. Exp.(%) Ag3333, Run 165084139 |
|-------------------------------|--|---|--|
| Secondary Th1 act | 0.8 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 3.0 | HUVEC IFN gamma | 0.5 |
| Secondary Tr1 act | 0.6 | HUVEC TNF alpha + IFN gamma | 0.8 |
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.5 | HUVEC IL-11 | 0.3 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 0.6 |
| Primary Th1 act | 5.7 | Lung Microvascular EC TNFalpha + IL-1beta | 0.4 |
| Primary Th2 act | 9.8 | Microvascular Dermal EC none | 0.0 |
| Primary Tr1 act | 3.8 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.4 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 1.1 |
| Primary Th2 rest | 0.4 | Small airway epithelium none | 1.9 |
| Primary Tr1 rest | 0.6 | Small airway epithelium TNFalpha + IL-1beta | 1.4 |
| CD45RA CD4 lymphocyte act | 4.1 | Coronery artery SMC rest | 1.7 |
| CD45RO CD4 lymphocyte act | 1.7 | Coronery artery SMC TNFalpha + IL-1beta | 1.2 |
| CD8 lymphocyte act | 1.4 | Astrocytes rest | 100.0 |
| Secondary CD8 lymphocyte rest | 7.4 | Astrocytes TNFalpha + IL-1beta | 59.9 |
| Secondary CD8 | 0.0 | KU-812 (Basophil) rest | 2.0 |

| | | | |
|-----------------------|-----|-------------------------|------|
| CD8 Th1 Th2 Tr1 anti- | 0.5 | CCD1106 (Keratinocytes) | 12.5 |
|-----------------------|-----|-------------------------|------|

| | | | |
|---------------------------------|------|--|------|
| CD95 CH11 | | none | |
| LAK cells rest | 0.5 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 6.2 |
| LAK cells IL-2 | 0.3 | Liver cirrhosis | 0.9 |
| LAK cells IL-2+IL-12 | 0.5 | Lupus kidney | 3.9 |
| LAK cells IL-2+IFN gamma | 0.0 | NCI-H292 none | 29.3 |
| LAK cells IL-2+ IL-18 | 0.6 | NCI-H292 IL-4 | 39.5 |
| LAK cells PMA/ionomycin | 0.3 | NCI-H292 IL-9 | 23.3 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 21.9 |
| Two Way MLR 3 day | 0.8 | NCI-H292 IFN gamma | 14.5 |
| Two Way MLR 5 day | 0.9 | HPAEC none | 0.5 |
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 4.5 |
| PBMC PWM | 8.1 | Lung fibroblast TNF alpha + IL-1 beta | 2.2 |
| PBMC PHA-L | 11.6 | Lung fibroblast IL-4 | 12.9 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 9.2 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 8.5 |
| B lymphocytes PWM | 15.4 | Lung fibroblast IFN gamma | 8.4 |
| B lymphocytes CD40L and IL-4 | 2.1 | Dermal fibroblast CCD1070 rest | 40.6 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 20.9 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 19.3 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 1.8 |
| Dendritic cells LPS | 0.5 | Dermal fibroblast IL-4 | 3.8 |
| Dendritic cells anti- CD40 | 0.0 | IBD Colitis 2 | 0.0 |
| Monocytes rest | 0.0 | IBD Crohn's | 2.5 |
| Monocytes LPS | 0.0 | Colon | 4.2 |
| Macrophages rest | 0.0 | Lung | 9.1 |
| Macrophages LPS | 0.0 | Thymus | 11.3 |
| HUVFC none | 0.4 | Kidney | 2.6 |

NS_neurodegeneration_v1.0 Summary: This panel contains the expression of this gene in the brain in an independent group of individuals. However, no differential expression of this

gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3333 This gene is expressed at moderate to low levels in many of the samples on this panel, with the highest expression in colon cancer cell line SW480 (CT=27.8). Expression is significantly lower in SW680, a cell line derived from a metastasis of the primary tumor represented by SW480. Thus, expression of this gene could be used to differentiate between these two cell lines and potentially between primary colon cancer and its metastases.

Based on expression in this panel, this gene may be involved in gastric, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes

This gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3333 The CG57789-01 gene is expressed at moderate to low levels in several samples on this panel, with the highest expression in resting astrocytes (CT=28.4). Moderate expression of this gene is seen in treated and untreated dermal and lung fibroblasts and the airway epithelial tumor line NCI-H292 cells. Thus, the transcript or the protein it encodes may be involved in pathological and inflammatory skin and lung conditions.

(+) CG57758-01 and (-) CG57758-02: SODIUM/LITHIUM-DEPENDENT DICARBOXYLATE TRANSPORTER

Expression of gene CG57758-01, a splice variant of CG57758-02, and CG57758-02 was assessed using the primer-probe sets Ag3326 and Ag3692, described in Tables QA and QB. Results of the RTQ-PCR runs are shown in Tables QC, QD, QE and QF.

Table QA. Probe Name Ag3326

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -ccatTTactggtgacagaagt-3' | 22 | 149 | 432 |
| Probe | TET-5' -atccctctggctgtcacctctcat-3' TAMRA | 26 | 172 | 433 |
| Reverse | 5' -ggagtccagaatctggaagagt-3' | 22 | 216 | 434 |

Table QB. Probe Name Ag3692

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -ccatTTactggtgacagaagt-3' | 22 | 149 | 435 |
| Probe | TET-5' -atccctctggctgtcacctctcat-3' TAMRA | 26 | 172 | 436 |
| Reverse | 5' -ggagtccagaatctggaagagt-3' | 22 | 216 | 437 |

Table QC. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3326, Run 210144197 | Rel. Exp.(%) Ag3692, Run 211145262 | Rel. Exp.(%) Ag3692, Run 224337942 | Tissue Name | Rel. Exp.(%) Ag3326, Run 210144197 | Rel. Exp.(%) Ag3692, Run 211145262 | Rel. Exp.(%) Ag3692, Run 224337942 |
|---------------|---|---|---|-------------------------------------|---|---|---|
| AD 1 Hippo | 2.1 | 4.3 | 1.0 | Control (Path) 3 Temporal Ctx | 8.5 | 15.3 | 12.0 |
| AD 2 Hippo | 20.9 | 28.3 | 25.0 | Control (Path) 4 Temporal Ctx | 31.2 | 36.6 | 52.1 |

| Sample | RTQ-PCR Run AD 4 | RTQ-PCR Run AD 2 | RTQ-PCR Run 0.0 | RTQ-PCR Run 0.0 |
|--------|------------------------|------------------------|-----------------------|-----------------------|
| | 2.1 | 7.1 | 2.6 | 0.0 |

| | | | | | | | |
|------------------------------|--------------|--------------|------|---|------|------|------|
| Hippo | | | | Occipital Ctx (Missing) | | | |
| AD 5 hippo | 72.7 | 97.9 | 85.3 | AD 3 Occipital Ctx | 1.5 | 7.2 | 1.3 |
| AD 6 Hippo | 13.7 | 18.3 | 5.5 | AD 4 Occipital Ctx | 71.7 | 35.6 | 30.6 |
| Control 2 Hippo | 14.5 | 20.2 | 15.2 | AD 5 Occipital Ctx | 25.3 | 31.9 | 12.4 |
| Control 4 Hippo | 11.7 | 7.4 | 5.1 | AD 6 Occipital Ctx | 17.2 | 19.1 | 11.2 |
| Control (Path) 3 Hippo | 6.7 | 4.4 | 4.5 | Control 1 Occipital Ctx | 7.0 | 9.0 | 8.1 |
| AD 1 Temporal Ctx | 4.0 | 1.7 | 2.8 | Control 2 Occipital Ctx | 33.2 | 44.8 | 26.1 |
| AD 2 Temporal Ctx | 80.7 | 50.7 | 37.4 | Control 3 Occipital Ctx | 30.1 | 37.6 | 21.9 |
| AD 3 Temporal Ctx | 3.6 | 0.0 | 1.1 | Control 4 Occipital Ctx | 16.3 | 12.6 | 8.2 |
| AD 4 Temporal Ctx | 19.5 | 30.6 | 15.2 | Control (Path) 1 Occipital Ctx | 42.0 | 55.9 | 52.9 |
| AD 5 Inf Temporal Ctx | 100.0 | 100.0 | 99.3 | Control (Path) 2 Occipital Ctx | 6.7 | 13.0 | 7.7 |
| AD 5 SupTemp oral Ctx | 32.8 | 29.1 | 33.2 | Control (Path) 3 Occipital Ctx | 8.7 | 6.6 | 5.4 |

| CMPD Ctx | | | Occipital Ctx | | | |
|----------|--|--|------------------|--|--|--|
| Ctx | | | Ctx | | | |

| | | | | | | | |
|-------------------------------|------|------|------|-------------------------------|------|------|--------------|
| AD 6 Sup Temporal Ctx | 41.8 | 53.6 | 17.0 | Control 1 Parietal Ctx | 21.2 | 23.0 | 15.3 |
| Control 1 Temporal Ctx | 12.0 | 33.9 | 18.3 | Control 2 Parietal Ctx | 48.6 | 38.2 | 22.1 |
| Control 2 Temporal Ctx | 30.1 | 49.3 | 44.4 | Control 3 Parietal Ctx | 28.3 | 34.4 | 32.8 |
| Control 3 Temporal Ctx | 38.7 | 39.5 | 33.4 | Control (Path) 1 Parietal Ctx | 78.5 | 97.3 | 100.0 |
| Control 4 Temporal Ctx | 17.6 | 25.2 | 24.1 | Control (Path) 2 Parietal Ctx | 50.7 | 50.7 | 37.9 |
| Control (Path) 1 Temporal Ctx | 69.7 | 70.7 | 49.7 | Control (Path) 3 Parietal Ctx | 10.7 | 10.1 | 9.6 |
| Control (Path) 2 Temporal Ctx | 35.4 | 50.7 | 33.4 | Control (Path) 4 Parietal Ctx | 30.6 | 24.5 | 40.9 |

Table QD. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3326, Run 215678613 | Rel. Exp.(%) Ag3692, Run 217131191 | Tissue Name | Rel. Exp.(%) Ag3326, Run 215678613 | Rel. Exp.(%) Ag3692, Run 217131191 |
|----------------------------|--|--|-------------------------------------|--|--|
| Adipose | 0.0 | 0.0 | Renal ca. TK-10 | 11.4 | 12.0 |
| Melanoma* Hs688(A).T | 0.0 | 0.0 | Bladder | 0.0 | 0.1 |
| Melanoma* Hs688(B).T | 0.1 | 0.0 | Gastric ca. (liver met.) NCI-N87 | 0.0 | 0.0 |
| Melanoma* M14 | 0.0 | 0.0 | Gastric ca. KATO III | 0.0 | 0.0 |
| Melanoma* LOXIMVI | 0.0 | 0.0 | Colon ca. SW- 048 | 0.0 | 0.0 |
| Squamous cell carcinoma | 0.9 | 0.7 | Colon ca. (SW480 met) | 0.0 | 0.0 |

| | | | | | |
|-------------------------------------|-----|-----|-------------------------------------|-----|-----|
| SCC-4 | | | SW620 | | |
| Testis Pool | 0.1 | 0.2 | Colon ca. HT29 | 0.0 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | 0.0 | Colon ca. HCT-116 | 0.0 | 0.0 |
| Prostate Pool | 0.0 | 0.0 | Colon ca. CaCo-2 | 0.0 | 0.0 |
| Placenta | 0.0 | 0.0 | Colon cancer tissue | 0.1 | 0.0 |
| Uterus Pool | 0.0 | 0.0 | Colon ca. SW1116 | 0.0 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.0 | 0.0 | Colon ca. Colo-205 | 0.0 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.0 | 0.0 | Colon ca. SW-48 | 0.0 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.1 | 0.0 | Colon Pool | 0.6 | 0.0 |
| Ovarian ca. OVCAR-5 | 0.0 | 0.0 | Small Intestine Pool | 0.1 | 0.0 |
| Ovarian ca. IGROV-1 | 0.0 | 0.0 | Stomach Pool | 0.0 | 0.0 |
| Ovarian ca. OVCAR-8 | 2.8 | 2.2 | Bone Marrow Pool | 0.0 | 0.1 |
| Ovary | 0.7 | 0.6 | Fetal Heart | 0.0 | 0.0 |
| Breast ca. MCF-7 | 0.0 | 0.0 | Heart Pool | 0.0 | 0.0 |
| Breast ca. MDA-MB-231 | 0.0 | 0.0 | Lymph Node Pool | 0.1 | 0.0 |
| Breast ca. BT 549 | 0.6 | 0.8 | Fetal Skeletal Muscle | 0.0 | 0.0 |
| Breast ca. T47D | 0.0 | 0.0 | Skeletal Muscle Pool | 0.0 | 0.0 |
| Breast ca. MDA-N | 0.0 | 0.0 | Spleen Pool | 0.4 | 0.2 |
| Breast Pool | 0.0 | 0.1 | Thymus Pool | 0.0 | 0.0 |
| Trachea | 0.2 | 0.1 | CNS cancer (glio/astro) U87-MG | 0.0 | 0.0 |
| Lung | 0.0 | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.0 | 0.0 |

| | | | | | |
|-------------------|-----|-----|------------------------------|-----|-----|
| Lung ca. NCI-N417 | 0.0 | 0.0 | CNS cancer (astro) SF-539 | 0.0 | 0.0 |
|-------------------|-----|-----|------------------------------|-----|-----|

| | | | | | |
|-------------------|--------------|--------------|-------------------------------|------|------|
| Lung ca. LX-1 | 0.0 | 0.0 | CNS cancer (astro) SNB-75 | 0.0 | 0.0 |
| Lung ca. NCI-H146 | 0.0 | 0.0 | CNS cancer (glio) SNB-19 | 0.0 | 0.0 |
| Lung ca. SHP-77 | 0.0 | 0.0 | CNS cancer (glio) SF-295 | 0.1 | 0.1 |
| Lung ca. A549 | 0.0 | 0.1 | Brain (Amygdala) Pool | 0.4 | 0.4 |
| Lung ca. NCI-H526 | 2.0 | 0.0 | Brain (cerebellum) | 1.4 | 1.0 |
| Lung ca. NCI-H23 | 0.7 | 0.6 | Brain (fetal) | 0.7 | 0.4 |
| Lung ca. NCI-H460 | 0.0 | 0.0 | Brain (Hippocampus) Pool | 0.5 | 0.7 |
| Lung ca. HOP-62 | 0.1 | 0.2 | Cerebral Cortex Pool | 1.4 | 1.5 |
| Lung ca. NCI-H522 | 0.0 | 0.0 | Brain (Substantia nigra) Pool | 1.4 | 1.4 |
| Liver | 28.7 | 24.1 | Brain (Thalamus) Pool | 1.1 | 0.9 |
| Fetal Liver | 100.0 | 100.0 | Brain (whole) | 4.1 | 3.7 |
| Liver ca. HepG2 | 29.5 | 26.2 | Spinal Cord Pool | 0.1 | 0.2 |
| Kidney Pool | 0.0 | 0.0 | Adrenal Gland | 2.6 | 1.9 |
| Fetal Kidney | 0.1 | 0.1 | Pituitary gland Pool | 0.0 | 0.2 |
| Renal ca. 786-0 | 0.0 | 0.0 | Salivary Gland | 40.9 | 35.1 |
| Renal ca. A498 | 0.0 | 0.0 | Thyroid (female) | 0.0 | 0.0 |
| Renal ca. ACHN | 0.0 | 0.0 | Pancreatic ca. CAPAN2 | 0.5 | 0.8 |
| Renal ca. UO-31 | 0.0 | 0.0 | Pancreas Pool | 0.0 | 0.0 |

Table QE. Panel 4.1D

| Tissue Name | Rel. Exp.(%) Ag3692, Run 169987356 | Tissue Name | Rel. Exp.(%) Ag3692, Run 169987356 |
|-------------|--|-------------|--|
|-------------|--|-------------|--|

| | | | |
|--------------------|-----|------------------------|-----|
| Secondary trit act | 0.0 | ILV C1 TNF alpha gamma | 0.0 |
|--------------------|-----|------------------------|-----|

| | | | |
|--------------------------------|-----|--|------|
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 0.0 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 11.3 |
| Primary Tr1 act | 4.2 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 28.5 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 5.7 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 3.9 | Coronery artery SMC rest | 0.0 |
| CD45RO CD4 lymphocyte act | 0.0 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 0.0 |
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 0.0 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 3.6 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 4.3 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 10.7 |
| LAK cells rest | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 94.0 |
| LAK cells IL-2+IL-12 | 0.0 | NCI-H292 none | 0.0 |
| LAK cells IL-2+IFN gamma | 0.0 | NCI-H292 IL-4 | 0.0 |
| LAK cells IL-2+ IL-18 | 0.0 | NCI-H292 IL-9 | 0.0 |
| LAK cells PMA/ionomycin | 0.0 | NCI-H292 IL-13 | 0.0 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IFN gamma | 0.0 |
| Two Way MLR 3 day | 0.0 | HPAEC none | 0.0 |

HPAEC TNF alpha + IL-1

| | | | |
|-----------|-----|---------------------------------------|-----|
| PBMC rest | 0.0 | Lung fibroblast IFN alpha + IL-1 beta | 0.0 |
|-----------|-----|---------------------------------------|-----|

| | | | |
|------------------------------|-----|-------------------------------------|--------------|
| PBMC PWM | 0.0 | Lung fibroblast IL-4 | 0.0 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-9 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-13 | 0.0 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes PWM | 0.0 | Dermal fibroblast CCD1070 rest | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells none | 0.0 | Dermal fibroblast IL-4 | 0.0 |
| Dendritic cells LPS | 0.0 | Dermal Fibroblasts rest | 0.0 |
| Dendritic cells anti-CD40 | 0.0 | Neutrophils TNFa+LPS | 0.0 |
| Monocytes rest | 0.0 | Neutrophils rest | 0.0 |
| Monocytes LPS | 0.0 | Colon | 0.0 |
| Macrophages rest | 0.0 | Lung | 0.0 |
| Macrophages LPS | 0.0 | Thymus | 2.4 |
| HUVEC none | 0.0 | Kidney | 100.0 |
| HUVEC starved | 0.0 | | |

Table QF. Panel 5 Islet

| Tissue Name | Rel. Exp.(%) Ag3326, Run 242385365 | Tissue Name | Rel. Exp.(%) Ag3326, Run 242385365 |
|------------------------------------|--|------------------------------|--|
| 97457_Patient-02go_adipose | 0.0 | 94709_Donor 2 AM - A_adipose | 0.2 |
| 97476_Patient-07sk_skeletal muscle | 0.0 | 94710_Donor 2 AM - B_adipose | 0.0 |
| 97477_Patient-07ut_uterus | 0.0 | 94711_Donor 2 AM - C_adipose | 0.0 |
| 97478_Patient-07pl_placenta | 0.0 | 94712_Donor 2 AD - A_adipose | 0.0 |
| 99167_Bayer Patient 1 | 0.3 | 94713_Donor 2 AD - B_adipose | 0.0 |
| 97482_Patient-08ut_uterus | 0.0 | 94714_Donor 2 AD - C_adipose | 0.0 |

97486_Patient-09sk_skeletal muscle

94745_Donor 2 B_Mesenchymal Stem Cells

| | | | |
|--|-----|---|-------|
| 97487_Patient-09ut_uterus | 0.0 | 94730_Donor 3 AM - A_adipose | 0.0 |
| 97488_Patient-09pl_placenta | 0.0 | 94731_Donor 3 AM - B_adipose | 0.0 |
| 97492_Patient-10ut_uterus | 0.0 | 94732_Donor 3 AM - C_adipose | 0.0 |
| 97493_Patient-10pl_placenta | 0.0 | 94733_Donor 3 AD - A_adipose | 0.0 |
| 97495_Patient-11go_adipose | 0.0 | 94734_Donor 3 AD - B_adipose | 0.0 |
| 97496_Patient-11sk_skeletal muscle | 0.0 | 94735_Donor 3 AD - C_adipose | 0.0 |
| 97497_Patient-11ut_uterus | 0.0 | 77138_Liver_HepG2untreated | 100.0 |
| 97498_Patient-11pl_placenta | 0.0 | 73556_Heart_Cardiac stromal cells (primary) | 0.0 |
| 97500_Patient-12go_adipose | 0.1 | 81735_Small Intestine | 39.5 |
| 97501_Patient-12sk_skeletal muscle | 0.3 | 72409_Kidney_Proximal Convoluted Tubule | 0.0 |
| 97502_Patient-12ut_uterus | 0.0 | 82685_Small intestine_Duodenum | 0.0 |
| 97503_Patient-12pl_placenta | 0.0 | 90650_Adrenal_Adrenocortical adenoma | 0.0 |
| 94721_Donor 2 U - A_Mesenchymal Stem Cells | 0.0 | 72410_Kidney_HRCE | 0.0 |
| 94722_Donor 2 U - B_Mesenchymal Stem Cells | 0.0 | 72411_Kidney_HRE | 0.0 |
| 94723_Donor 2 U - C_Mesenchymal Stem Cells | 0.0 | 73139_Uterus_Uterine smooth muscle cells | 0.0 |

CNS_neurodegeneration_v1.0 Summary: Ag3326/Ag3692 - Three experiments done with two primer pairs (same sequence) are in excellent agreement. This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system

General_screening_panel_v1.4 Summary: Ag3326/Ag3692 Two experiments with the smae probe and primer set produce results that are in excellent agreement. This gene is highly expressed in fetal liver (CT=26.5-27.0) and moderately expressed in adult liver (CT=28.5-28.8) and liver cancer cell line HepG2 (CT=28.4-28.8). This result agrees with the results seen in Panel 5 (expression in HepG2 (CT=29.2). These results are in agreement with published data that show a novel sodium dicarboxylate transporter in brain, choroid plexus kidney, intestine and liver. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker for liver derived tissue.

This gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, and cerebral cortex. Therefore, this gene may play a role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Low but significant levels of expression are also seen in the adrenal gland. Thus, this gene product may also be involved in metabolic disorders of this gland, including adrenoleukodystrophy and congenital adrenal hyperplasia.

References:

1. Pajor AM, Gangula R, Yao X. Cloning and functional characterization of a high-affinity Na(+)/dicarboxylate cotransporter from mouse brain. Am J Physiol Cell Physiol 2001 May;280(5):C1215-23.
2. Chen XZ, Shayakul C, Berger UV, Tian W, Hediger MA. Characterization of a rat Na+-dicarboxylate cotransporter. J Biol Chem 1998 Aug 14;273(33):20972-81.

Panel 4.1D Summary: Ag3692 Significant expression of this gene is seen only in kidney and a liver cirrhosis sample (CTs=34.0). These results confirm that this gene is expressed in liver derived samples. The presence in the kidney is also in agreement with published results.

Please see Panel 1.4. This gene product may be involved in maintaining or restoring normal function to the kidney during inflammation.

Panel 5 Islet Summary: Ag3326 - The highest expression of this gene is in liver cancer cell line HepG2 (CT=29.2). There is also moderate expression in the small intestine (CT=30.5). These results compare well with previously published reports of sodium dicarboxylate transporter expression in mouse and rat (see discussion Panel 1.4).

R. CG57758-04 and CG57758-05: Sodium:sulfate symporter

Expression of gene CG57758-04 and CG57758-05, both splice variants of CG577584-01, was assessed using the primer-probe sets Ag3326, Ag3692 and Ag5818, described in Tables RA, RB and RC. Results of the RTQ-PCR runs are shown in Tables RD, RE, RF, RG and RH.

Table RA. Probe Name Ag3326

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-ccatTTactggtgacagaagt-3' | 22 | 138 | 438 |
| Probe | TET-5'-atccctctggctgtcacctctcat-3' - TAMRA | 26 | 161 | 439 |
| Reverse | 5'-ggagtccagaatctggaagagt-3' | 22 | 205 | 440 |

Table RB. Probe Name Ag3692

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-ccatTTactggtgacagaagt-3' | 22 | 138 | 441 |
| Probe | TET-5'-atccctctggctgtcacctctcat-3' - TAMRA | 26 | 161 | 442 |
| Reverse | 5'-ggagtccagaatctggaagagt-3' | 22 | 205 | 443 |

Table RC. Probe Name Ag5818

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-ccatcaccttgcattgtcc-3' | 20 | 1341 | 444 |
| Probe | TET-5'-ttatgactcctgtttcacatggaggca- 3' -TAMRA | 29 | 1429 | 445 |
| Reverse | 5'-cagaagactccaattatgttca-3' | 22 | 1458 | 446 |

| Tissue Name | Rei. Exp.(%) | Rel. Exp.(%) | Rei. Exp.(%) | Tissue Name | Rei. Exp.(%) | Rel. Exp.(%) | Rei. Exp.(%) |
|-------------|--------------|--------------|--------------|-------------|--------------|--------------|--------------|
| | | | | | | | |

| | Ag3326, Run 210144197 | Ag3692, Run 211145262 | Ag3692, Run 224337942 | | Ag3326, Run 210144197 | Ag3692, Run 211145262 | Ag3692, Run 224337942 |
|------------------------------|-----------------------------|-----------------------------|-----------------------------|-------------------------------------|-----------------------------|-----------------------------|-----------------------------|
| AD 1 Hippo | 2.1 | 4.3 | 1.0 | Control (Path) 3 Temporal Ctx | 8.5 | 15.3 | 12.0 |
| AD 2 Hippo | 20.9 | 28.3 | 25.0 | Control (Path) 4 Temporal Ctx | 31.2 | 36.6 | 52.1 |
| AD 3 Hippo | 0.0 | 0.9 | 0.6 | AD 1 Occipital Ctx | 2.7 | 3.0 | 0.0 |
| AD 4 Hippo | 2.1 | 7.1 | 2.6 | AD 2 Occipital Ctx (Missing) | 0.0 | 0.0 | 0.0 |
| AD 5 hippo | 72.7 | 97.9 | 85.3 | AD 3 Occipital Ctx | 1.5 | 7.2 | 1.3 |
| AD 6 Hippo | 13.7 | 18.3 | 5.5 | AD 4 Occipital Ctx | 71.7 | 35.6 | 30.6 |
| Control 2 Hippo | 14.5 | 20.2 | 15.2 | AD 5 Occipital Ctx | 25.3 | 31.9 | 12.4 |
| Control 4 Hippo | 11.7 | 7.4 | 5.1 | AD 6 Occipital Ctx | 17.2 | 19.1 | 11.2 |
| Control (Path) 3 Hippo | 6.7 | 4.4 | 4.5 | Control 1 Occipital Ctx | 7.0 | 9.0 | 8.1 |
| AD 1 Temporal Ctx | 4.0 | 1.7 | 2.8 | Control 2 Occipital Ctx | 33.2 | 44.8 | 26.1 |
| AD 2 Temporal Ctx | 80.7 | 50.7 | 37.4 | Control 3 Occipital Ctx | 30.1 | 37.6 | 21.9 |

| | | | | | | | |
|------|------|------|------|---------|------|------|------|
| AD 4 | 19.5 | 30.6 | 15.2 | Control | 42.0 | 55.9 | 52.9 |
|------|------|------|------|---------|------|------|------|

| | | | | | | | |
|-------------------------------|-------|-------|------|-----------------------------------|------|------|-------|
| Temporal Ctx | | | | (Path) 1 Occipital Ctx | | | |
| AD 5 Inf Temporal Ctx | 100.0 | 100.0 | 99.3 | Control (Path) 2 Occipital Ctx | 6.7 | 13.0 | 7.7 |
| AD 5 SupTemporal Ctx | 32.8 | 29.1 | 33.2 | Control (Path) 3 Occipital Ctx | 8.7 | 6.6 | 5.4 |
| AD 6 Inf Temporal Ctx | 27.7 | 21.3 | 26.6 | Control (Path) 4 Occipital Ctx | 8.1 | 9.0 | 7.4 |
| AD 6 Sup Temporal Ctx | 41.8 | 53.6 | 17.0 | Control 1 Parietal Ctx | 21.2 | 23.0 | 15.3 |
| Control 1 Temporal Ctx | 12.0 | 33.9 | 18.3 | Control 2 Parietal Ctx | 48.6 | 38.2 | 22.1 |
| Control 2 Temporal Ctx | 30.1 | 49.3 | 44.4 | Control 3 Parietal Ctx | 28.3 | 34.4 | 32.8 |
| Control 3 Temporal Ctx | 38.7 | 39.5 | 33.4 | Control (Path) 1 Parietal Ctx | 78.5 | 97.3 | 100.0 |
| Control 4 Temporal Ctx | 17.6 | 25.2 | 24.1 | Control (Path) 2 Parietal Ctx | 50.7 | 50.7 | 37.9 |
| Control (Path) 1 Temporal Ctx | 69.7 | 70.7 | 49.7 | Control (Path) 3 Parietal Ctx | 10.7 | 10.1 | 9.6 |
| Control (Path) 2 Temporal Ctx | 35.4 | 50.7 | 33.4 | Control (Path) 4 Parietal Ctx | 30.6 | 24.5 | 40.9 |

| Tissue Name | Rel. Exp.(%) | Rel. Exp.(%) | Tissue Name | Rel. Exp.(%) | Rel. Exp.(%) |
|-------------|--------------|--------------|-------------|--------------|--------------|
|-------------|--------------|--------------|-------------|--------------|--------------|

| | Ag3326, Run 215678613 | Ag3692, Run 217131191 | | Ag3326, Run 215678613 | Ag3692, Run 217131191 |
|-------------------------------------|----------------------------------|----------------------------------|-------------------------------------|----------------------------------|----------------------------------|
| Adipose | 0.0 | 0.0 | Renal ca. TK-10 | 11.4 | 12.0 |
| Melanoma* Hs688(A).T | 0.0 | 0.0 | Bladder | 0.0 | 0.1 |
| Melanoma* Hs688(B).T | 0.1 | 0.0 | Gastric ca. (liver met.) NCI-N87 | 0.0 | 0.0 |
| Melanoma* M14 | 0.0 | 0.0 | Gastric ca. KATO III | 0.0 | 0.0 |
| Melanoma* LOXIMVI | 0.0 | 0.0 | Colon ca. SW- 948 | 0.0 | 0.0 |
| Melanoma* SK-MEL-5 | 0.0 | 0.0 | Colon ca. SW480 | 0.0 | 0.0 |
| Squamous cell carcinoma SCC-4 | 0.9 | 0.7 | Colon ca.* (SW480 met) SW620 | 0.0 | 0.0 |
| Testis Pool | 0.1 | 0.2 | Colon ca. HT29 | 0.0 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | 0.0 | Colon ca. HCT- 116 | 0.0 | 0.0 |
| Prostate Pool | 0.0 | 0.0 | Colon ca. CaCo-2 | 0.0 | 0.0 |
| Placenta | 0.0 | 0.0 | Colon cancer tissue | 0.1 | 0.0 |
| Uterus Pool | 0.0 | 0.0 | Colon ca. SW1116 | 0.0 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.0 | 0.0 | Colon ca. Colo- 205 | 0.0 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.0 | 0.0 | Colon ca. SW-48 | 0.0 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.1 | 0.0 | Colon Pool | 0.6 | 0.0 |
| Ovarian ca. OVCAR-5 | 0.0 | 0.0 | Small Intestine Pool | 0.1 | 0.0 |
| Ovarian ca. IGROV-1 | 0.0 | 0.0 | Stomach Pool | 0.0 | 0.0 |
| Ovarian ca. OVCAR-8 | 2.8 | 2.2 | Bone Marrow Pool | 0.0 | 0.1 |
| Ovary | 0.7 | 0.6 | Fetal Heart | 0.0 | 0.0 |
| Breast ca. MCF-7 | 0.0 | 0.0 | Heart Pool | 0.0 | 0.0 |
| Breast ca. MDA-MB-231 | | | Lymph Node | | |

| | | | | | |
|---------------------|-------|-------|-------------------------------------|-----|-----|
| Breast ca. T47D | 0.0 | 0.0 | Skeletal Muscle Pool | 0.0 | 0.0 |
| Breast ca. MDA-N | 0.0 | 0.0 | Spleen Pool | 0.4 | 0.2 |
| Breast Pool | 0.0 | 0.1 | Thymus Pool | 0.0 | 0.0 |
| Trachea | 0.2 | 0.1 | CNS cancer (glio/astro) U87-MG | 0.0 | 0.0 |
| Lung | 0.0 | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.0 | 0.0 |
| Fetal Lung | 0.2 | 0.1 | CNS cancer (neuro;met) SK-N-AS | 0.0 | 0.0 |
| Lung ca. NCI-N417 | 0.0 | 0.0 | CNS cancer (astro) SF-539 | 0.0 | 0.0 |
| Lung ca. LX-1 | 0.0 | 0.0 | CNS cancer (astro) SNB-75 | 0.0 | 0.0 |
| Lung ca. NCI-H146 | 0.0 | 0.0 | CNS cancer (glio) SNB-19 | 0.0 | 0.0 |
| Lung ca. SHP-77 | 0.0 | 0.0 | CNS cancer (glio) SF-295 | 0.1 | 0.1 |
| Lung ca. A549 | 0.0 | 0.1 | Brain (Amygdala) Pool | 0.4 | 0.4 |
| Lung ca. NCI-H526 | 2.0 | 0.0 | Brain (cerebellum) | 1.4 | 1.0 |
| Lung ca. NCI-H23 | 0.7 | 0.6 | Brain (fetal) | 0.7 | 0.4 |
| Lung ca. NCI-H460 | 0.0 | 0.0 | Brain (Hippocampus) Pool | 0.5 | 0.7 |
| Lung ca. HOP-62 | 0.1 | 0.2 | Cerebral Cortex Pool | 1.4 | 1.5 |
| Lung ca. NCI-H522 | 0.0 | 0.0 | Brain (Substantia nigra) Pool | 1.4 | 1.4 |
| Liver | 28.7 | 24.1 | Brain (Thalamus) Pool | 1.1 | 0.9 |
| Fetal Liver | 100.0 | 100.0 | Brain (whole) | 4.1 | 3.7 |
| Liver ca. HepG2 | 29.5 | 26.2 | Spinal Cord Pool | 0.1 | 0.2 |
| Kidney Pool | 0.0 | 0.0 | Adrenal Gland | 2.6 | 1.9 |

Pituitary gland

| | | | | | |
|-----------|-----|-----|------------------|-----|-----|
| Renal ca. | 0.0 | 0.0 | Thyroid (female) | 0.0 | 0.0 |
|-----------|-----|-----|------------------|-----|-----|

| | | | | | |
|---------------------|-----|-----|--------------------------|-----|-----|
| A498 | | | | | |
| Renal ca. ACHN | 0.0 | 0.0 | Pancreatic ca. CAPAN2 | 0.5 | 0.8 |
| Renal ca. UO- 31 | 0.0 | 0.0 | Pancreas Pool | 0.0 | 0.0 |

Table RF. General_screening_panel_v1.5

| Tissue Name | Rel. Exp.(%) Ag5818, Run 245382899 | Tissue Name | Rel. Exp.(%) Ag5818, Run 245382899 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 0.0 | Renal ca. TK-10 | 13.4 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 0.0 |
| Melanoma* Hs688(B).T | 0.0 | Gastric ca. (liver met.) NCI-N87 | 0.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 0.0 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |
| Melanoma* SK- MEL-5 | 0.0 | Colon ca. SW480 | 0.0 |
| Squamous cell carcinoma SCC-4 | 1.4 | Colon ca.* (SW480 met) SW620 | 0.0 |
| Testis Pool | 0.5 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 0.0 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 0.4 |
| Placenta | 0.0 | Colon cancer tissue | 0.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.0 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV- 3 | 0.1 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.0 | Colon Pool | 0.0 |
| Ovarian ca. OVCAR-5 | 0.0 | Small Intestine Pool | 0.0 |
| Ovarian ca. IGROV- 1 | 0.0 | Stomach Pool | 0.0 |
| Ovarian ca. OVCAR-8 | 1.9 | Bone Marrow Pool | 0.0 |
| Ovary | 0.3 | Fetal Heart | 0.0 |

| | | | |
|-------------------|--------------|-------------------------------------|------|
| Breast ca. BT 549 | 0.4 | Fetal Skeletal Muscle | 0.0 |
| Breast ca. T47D | 0.0 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 0.7 |
| Breast Pool | 0.0 | Thymus Pool | 0.0 |
| Trachea | 0.2 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.0 |
| Fetal Lung | 0.2 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 0.0 | CNS cancer (astro) SNB-75 | 0.0 |
| Lung ca. NCI-H146 | 0.0 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 0.0 | CNS cancer (glio) SF-295 | 0.0 |
| Lung ca. A549 | 0.2 | Brain (Amygdala) Pool | 0.7 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 1.1 |
| Lung ca. NCI-H23 | 1.5 | Brain (fetal) | 0.8 |
| Lung ca. NCI-H460 | 0.0 | Brain (Hippocampus) Pool | 0.6 |
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 1.7 |
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) Pool | 1.2 |
| Liver | 40.3 | Brain (Thalamus) Pool | 1.3 |
| Fetal Liver | 100.0 | Brain (whole) | 5.6 |
| Liver ca. HepG2 | 33.2 | Spinal Cord Pool | 0.3 |
| Kidney Pool | 0.0 | Adrenal Gland | 6.0 |
| Fetal Kidney | 0.0 | Pituitary gland Pool | 0.2 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 67.4 |
| Renal ca. A498 | 0.0 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 0.7 |
| Renal ca. UO-31 | 0.0 | Pancreas Pool | 0.0 |

Table RG. Panel 4.1D

| | Rel. Exp.(%) | Rel. Exp.(%) | | Rel. Exp.(%) | Rel. Exp.(%) |
|-------------------|-----------------|-----------------|----------------|-----------------|-----------------|
| | 169987356 | 246920287 | | 169987356 | 246920287 |
| Secondary Th1 act | 0.0 | 0.0 | HUVEC IL-1beta | 0.0 | 0.0 |

| | | | | | |
|-------------------------------|-----|-----|---|------|------|
| Secondary Th2 act | 0.0 | 0.0 | HUVEC IFN gamma | 0.0 | 0.0 |
| Secondary Tr1 act | 0.0 | 0.0 | HUVEC TNF alpha + IFN gamma | 0.0 | 0.0 |
| Secondary Th1 rest | 0.0 | 0.0 | HUVEC TNF alpha + IL4 | 0.0 | 0.0 |
| Secondary Th2 rest | 0.0 | 0.0 | HUVEC IL-11 | 0.0 | 0.0 |
| Secondary Tr1 rest | 0.0 | 0.0 | Lung Microvascular EC none | 0.0 | 0.0 |
| Primary Th1 act | 0.0 | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 | 0.0 |
| Primary Th2 act | 0.0 | 0.0 | Microvascular Dermal EC none | 11.3 | 0.0 |
| Primary Tr1 act | 4.2 | 0.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 | 0.0 |
| Primary Th1 rest | 0.0 | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 28.5 | 0.0 |
| Primary Th2 rest | 0.0 | 0.0 | Small airway epithelium none | 5.7 | 0.0 |
| Primary Tr1 rest | 0.0 | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 | 0.0 |
| CD45RA CD4 lymphocyte act | 3.9 | 0.0 | Coronery artery SMC rest | 0.0 | 0.0 |
| CD45RO CD4 lymphocyte act | 0.0 | 0.0 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 | 0.0 |
| CD8 lymphocyte act | 0.0 | 0.0 | Astrocytes rest | 0.0 | 0.0 |
| Secondary CD8 lymphocyte rest | 0.0 | 0.0 | Astrocytes TNFalpha + IL-1beta | 0.0 | 0.0 |
| Secondary CD8 lymphocyte act | 0.0 | 0.0 | KU-812 (Basophil) rest | 3.6 | 24.3 |

| OTC | PMA (0.001μg/ml) | CCD1106 | 10.7 | 0.0 |
|-----|------------------|---------|------|-----|
| 2ry | 0.0 | 0.0 | | |

| | | | | | |
|------------------------------|-----|-----|---|------|------|
| Th1/Th2/Tr1 anti-CD95 CH11 | | | (Keratinocytes) none | | |
| LAK cells rest | 0.0 | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 | 0.0 |
| LAK cells IL-2 | 0.0 | 0.0 | Liver cirrhosis | 94.0 | 27.5 |
| LAK cells IL-2+IL-12 | 0.0 | 0.0 | NCI-H292 none | 0.0 | 0.0 |
| LAK cells IL-2+IFN gamma | 0.0 | 0.0 | NCI-H292 IL-4 | 0.0 | 0.0 |
| LAK cells IL-2+IL-18 | 0.0 | 0.0 | NCI-H292 IL-9 | 0.0 | 0.0 |
| LAK cells PMA/ionomycin | 0.0 | 0.0 | NCI-H292 IL-13 | 0.0 | 0.0 |
| NK Cells IL-2 rest | 0.0 | 0.0 | NCI-H292 IFN gamma | 0.0 | 0.0 |
| Two Way MLR 3 day | 0.0 | 0.0 | HPAEC none | 0.0 | 0.0 |
| Two Way MLR 5 day | 3.2 | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.0 | 0.0 |
| Two Way MLR 7 day | 0.0 | 0.0 | Lung fibroblast none | 0.0 | 0.0 |
| PBMC rest | 0.0 | 0.0 | Lung fibroblast TNF alpha + IL-1 beta | 0.0 | 0.0 |
| PBMC PWM | 0.0 | 0.0 | Lung fibroblast IL-4 | 0.0 | 0.0 |
| PBMC PHA-L | 0.0 | 0.0 | Lung fibroblast IL-9 | 0.0 | 0.0 |
| Ramos (B cell) none | 0.0 | 0.0 | Lung fibroblast IL-13 | 0.0 | 0.0 |
| Ramos (B cell) ionomycin | 0.0 | 0.0 | Lung fibroblast IFN gamma | 0.0 | 0.0 |
| B lymphocytes PWM | 0.0 | 0.0 | Dermal fibroblast CCD1070 rest | 0.0 | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 | 0.0 |
| EOL-1 dbcAMP | 0.0 | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 | 0.0 |

| | | | | | |
|----------------------|-----|-----|------------------------|-----|-----|
| Dendritic cells none | 0.0 | 0.0 | Dermal fibroblast IL-4 | 0.0 | 0.0 |
|----------------------|-----|-----|------------------------|-----|-----|

| | | | | | |
|---------------------------|-----|-----|-------------------------|-------|-------|
| Dendritic cells LPS | 0.0 | 0.0 | Dermal Fibroblasts rest | 0.0 | 0.0 |
| Dendritic cells anti-CD40 | 0.0 | 0.0 | Neutrophils TNFa+LPS | 0.0 | 0.0 |
| Monocytes rest | 0.0 | 0.0 | Neutrophils rest | 0.0 | 0.0 |
| Monocytes LPS | 0.0 | 0.0 | Colon | 0.0 | 0.0 |
| Macrophages rest | 0.0 | 0.0 | Lung | 0.0 | 0.0 |
| Macrophages LPS | 0.0 | 0.0 | Thymus | 2.4 | 0.0 |
| HUVEC none | 0.0 | 0.0 | Kidney | 100.0 | 100.0 |
| HUVEC starved | 0.0 | 0.0 | | | |

Table RH. Panel 5 Islet

| Tissue Name | Rel. Exp.(%) Ag3326, Run 242385365 | Tissue Name | Rel. Exp.(%) Ag3326, Run 242385365 |
|------------------------------------|--|--|--|
| 97457_Patient-02go_adipose | 0.0 | 94709_Donor 2 AM - A_adipose | 0.2 |
| 97476_Patient-07sk_skeletal muscle | 0.0 | 94710_Donor 2 AM - B_adipose | 0.0 |
| 97477_Patient-07ut_uterus | 0.0 | 94711_Donor 2 AM - C_adipose | 0.0 |
| 97478_Patient-07pl_placenta | 0.0 | 94712_Donor 2 AD - A_adipose | 0.0 |
| 99167_Bayer Patient 1 | 0.3 | 94713_Donor 2 AD - B_adipose | 0.0 |
| 97482_Patient-08ut_uterus | 0.0 | 94714_Donor 2 AD - C_adipose | 0.0 |
| 97483_Patient-08pl_placenta | 0.0 | 94742_Donor 3 U - A_Mesenchymal Stem Cells | 0.0 |
| 97486_Patient-09sk_skeletal muscle | 0.0 | 94743_Donor 3 U - B_Mesenchymal Stem Cells | 0.0 |
| 97487_Patient-09ut_uterus | 0.0 | 94730_Donor 3 AM - A_adipose | 0.0 |
| 97488_Patient-09pl_placenta | 0.0 | 94731_Donor 3 AM - B_adipose | 0.0 |
| 97492_Patient-10ut_uterus | 0.0 | 94732_Donor 3 AM - C_adipose | 0.0 |
| 97493_Patient-10pl_placenta | 0.0 | 94733_Donor 3 AD - A_adipose | 0.0 |
| 97495_Patient-11go_adipose | 0.0 | 94734_Donor 3 AD - B_adipose | 0.0 |
| 97497_Patient-11ut_uterus | 0.0 | 97138_Liver HepG2untreated | 100.0 |

| | | | |
|--|-----|---|------|
| 97498_Patient-11pl_placenta | 0.0 | 73556_Heart_Cardiac stromal cells (primary) | 0.0 |
| 97500_Patient-12go_adipose | 0.1 | 81735_Small Intestine | 39.5 |
| 97501_Patient-12sk_skeletal muscle | 0.3 | 72409_Kidney_Proximal Convoluted Tubule | 0.0 |
| 97502_Patient-12ut_uterus | 0.0 | 82685_Small intestine_Duodenum | 0.0 |
| 97503_Patient-12pl_placenta | 0.0 | 90650_Adrenal_Adrenocortical adenoma | 0.0 |
| 94721_Donor 2 U - A_Mesenchymal Stem Cells | 0.0 | 72410_Kidney_HRCE | 0.0 |
| 94722_Donor 2 U - B_Mesenchymal Stem Cells | 0.0 | 72411_Kidney_HRE | 0.0 |
| 94723_Donor 2 U - C_Mesenchymal Stem Cells | 0.0 | 73139_Uterus_Uterine smooth muscle cells | 0.0 |

CNS_neurodegeneration_v1.0 Summary: Ag3326/Ag3692 - Three experiments done with two primer pairs (same sequence) are in excellent agreement. This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders. Ag5818 Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag3326/Ag3692 Two experiments with the same probe and primer set produce results that are in excellent agreement. This gene is highly expressed in fetal liver (CT=26.5-27.0) and moderately expressed in adult liver (CT=28.5-28.8) and liver cancer cell line HepG2 (CT=28.4-28.8). This result agrees with the results seen in Panel 5 (expression in HepG2 (CT=29.2). These results are in agreement with published data that show a novel sodium dicarboxylate transporter in brain, choroid plexus kidney, intestine and liver. Thus, expression of this gene could be used to differentiate between these

two types of tissue samples as well as a marker for liver derived tissue

substantia nigra, thalamus, cerebellum, and cerebral cortex. Therefore, this gene may play a

role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Low but significant levels of expression are also seen in the adrenal gland. Thus, this gene product may also be involved in metabolic disorders of this gland, including adrenoleukodystrophy and congenital adrenal hyperplasia.

References:

1. Pajor AM, Gangula R, Yao X. Cloning and functional characterization of a high-affinity Na(+) / dicarboxylate cotransporter from mouse brain. Am J Physiol Cell Physiol 2001 May;280(5):C1215-23.
2. Chen XZ, Shayakul C, Berger UV, Tian W, Hediger MA. Characterization of a rat Na+-dicarboxylate cotransporter. J Biol Chem 1998 Aug 14;273(33):20972-81.

General_screening_panel_v1.5 Summary: Ag5818 Results using this primer pair are in excellent agreement with the results seen in panel 1.4. See Panel 1.4 for discussion.

Panel 4.1D Summary: Ag3692 Significant expression of this gene is seen only in kidney and a liver cirrhosis sample (CTs=34.0). These results confirm that this gene is expressed in liver derived samples. The presence in the kidney is also in agreement with published results. Please see Panel 1.4. This gene product may be involved in maintaining or restoring normal function to the kidney during inflammation.

Panel 4D Summary: Ag3326 Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 5 Islet Summary: Ag3326 The highest expression of this gene is in liver cancer cell line HepG2 (CT=29.2). There is also moderate expression in the small intestine (CT=30.5). These results compare well with previously published reports of sodium dicarboxylate transporter expression in mouse and rat (see discussion Panel 1.4).

S. CG57732-01 and CG57732-02 and CG57732-03: CA2+/CALMODULIN-

EXPRESSION OF THESE GENES WAS ASSESSED IN THE R1Q ASSAY. EXPRESSION OF THE CALMODULIN GENE WAS ASSESSED USING THE PRIMER-PROBE SET AG3317, DESCRIBED IN TABLE SA. RESULTS OF THE R1Q-

PCR runs are shown in Tables SB, SC and SD. Please note CG57732-03 represents a splice variant of CG57732-01.

Table SA. Probe Name Ag3317

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-ggcctacaacgaaagtgaaga-3' | 21 | 451 | 447 |
| Probe | TET-5'-cagacactatgcaatgaaagtcccttcca- 3'-TAMRA | 29 | 472 | 448 |
| Reverse | 5'-ggaaagccatactgcttcagta-3' | 22 | 510 | 449 |

Table SB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3317, Run 210144081 | Tissue Name | Rel. Exp.(%) Ag3317, Run 210144081 |
|--------------------------|---------------------------------------|-----------------------------------|--|
| AD 1 Hippo | 10.7 | Control (Path) 3 Temporal Ctx | 4.1 |
| AD 2 Hippo | 23.7 | Control (Path) 4 Temporal Ctx | 42.6 |
| AD 3 Hippo | 4.5 | AD 1 Occipital Ctx | 12.5 |
| AD 4 Hippo | 7.5 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 hippo | 97.9 | AD 3 Occipital Ctx | 5.4 |
| AD 6 Hippo | 25.7 | AD 4 Occipital Ctx | 18.4 |
| Control 2 Hippo | 24.8 | AD 5 Occipital Ctx | 21.8 |
| Control 4 Hippo | 4.3 | AD 6 Occipital Ctx | 58.6 |
| Control (Path) 3 Hippo | 2.8 | Control 1 Occipital Ctx | 1.5 |
| AD 1 Temporal Ctx | 10.4 | Control 2 Occipital Ctx | 94.0 |
| AD 2 Temporal Ctx | 35.8 | Control 3 Occipital Ctx | 21.5 |
| AD 3 Temporal Ctx | 5.8 | Control 4 Occipital Ctx | 2.6 |
| AD 4 Temporal Ctx | 23.2 | Control (Path) 1 Occipital Ctx | 100.0 |
| AD 5 Inf Temporal Ctx | 88.9 | Control (Path) 2 Occipital Ctx | 13.8 |

| | |
|-----------------------------------|-----------------------------------|
| AD 1 Temporal Ctx | Control (Path) 1 Occipital Ctx |
| Control (Path) 2 Occipital Ctx | AD 1 Temporal Ctx |

| | | | |
|-------------------------------|------|-------------------------------|------|
| AD 6 Sup Temporal Ctx | 47.3 | Control 1 Parietal Ctx | 4.9 |
| Control 1 Temporal Ctx | 4.4 | Control 2 Parietal Ctx | 33.0 |
| Control 2 Temporal Ctx | 63.3 | Control 3 Parietal Ctx | 27.4 |
| Control 3 Temporal Ctx | 20.4 | Control (Path) 1 Parietal Ctx | 95.9 |
| Control 4 Temporal Ctx | 8.7 | Control (Path) 2 Parietal Ctx | 24.5 |
| Control (Path) 1 Temporal Ctx | 77.4 | Control (Path) 3 Parietal Ctx | 2.0 |
| Control (Path) 2 Temporal Ctx | 38.7 | Control (Path) 4 Parietal Ctx | 51.8 |

Table SC. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3317, Run 215678602 | Tissue Name | Rel. Exp.(%) Ag3317, Run 215678602 |
|-------------------------------|------------------------------------|----------------------------------|------------------------------------|
| Adipose | 2.4 | Renal ca. TK-10 | 14.2 |
| Melanoma* Hs688(A).T | 6.2 | Bladder | 10.5 |
| Melanoma* Hs688(B).T | 7.9 | Gastric ca. (liver met.) NCI-N87 | 22.2 |
| Melanoma* M14 | 18.2 | Gastric ca. KATO III | 23.0 |
| Melanoma* LOXIMVI | 9.4 | Colon ca. SW-948 | 11.1 |
| Melanoma* SK-MEL-5 | 9.8 | Colon ca. SW480 | 20.9 |
| Squamous cell carcinoma SCC-4 | 1.6 | Colon ca.* (SW480 met) SW620 | 21.6 |
| Testis Pool | 13.1 | Colon ca. HT29 | 11.3 |
| Prostate ca.* (bone met) PC-3 | 6.4 | Colon ca. HCT-116 | 27.0 |
| Prostate Pool | 3.1 | Colon ca. CaCo-2 | 1.6 |
| Placenta | 1.8 | Colon cancer tissue | 11.3 |
| Uterus Pool | 3.9 | Colon ca. SW1116 | 9.7 |
| Ovarian ca. OVCAR-3 | 11.6 | Colon ca. Colo-205 | 1.7 |
| Ovarian ca. SK-OV- | 18.7 | Colon ca. SW-48 | 8.8 |

| | | | |
|--------------------|------|----------------------|------|
| Ovarian ca OVCAR-5 | 17.2 | Small Intestine Pool | 21.2 |
|--------------------|------|----------------------|------|

| | | | |
|-----------------------|------|-------------------------------------|--------------|
| Ovarian ca. IGROV-1 | 6.2 | Stomach Pool | 5.3 |
| Ovarian ca. OVCAR-8 | 4.7 | Bone Marrow Pool | 5.1 |
| Ovary | 2.9 | Fetal Heart | 6.8 |
| Breast ca. MCF-7 | 6.1 | Heart Pool | 5.4 |
| Breast ca. MDA-MB-231 | 20.3 | Lymph Node Pool | 13.4 |
| Breast ca. BT 549 | 7.4 | Fetal Skeletal Muscle | 2.6 |
| Breast ca. T47D | 37.9 | Skeletal Muscle Pool | 2.3 |
| Breast ca. MDA-N | 9.0 | Spleen Pool | 2.8 |
| Breast Pool | 12.0 | Thymus Pool | 9.0 |
| Trachea | 17.2 | CNS cancer (glio/astro) U87-MG | 66.4 |
| Lung | 0.7 | CNS cancer (glio/astro) U-118-MG | 53.2 |
| Fetal Lung | 6.0 | CNS cancer (neuro;met) SK-N-AS | 4.6 |
| Lung ca. NCI-N417 | 16.5 | CNS cancer (astro) SF-539 | 17.2 |
| Lung ca. LX-1 | 20.9 | CNS cancer (astro) SNB-75 | 21.5 |
| Lung ca. NCI-H146 | 7.0 | CNS cancer (glio) SNB-19 | 5.1 |
| Lung ca. SHP-77 | 23.0 | CNS cancer (glio) SF-295 | 12.2 |
| Lung ca. A549 | 23.7 | Brain (Amygdala) Pool | 46.3 |
| Lung ca. NCI-H526 | 4.4 | Brain (cerebellum) | 92.7 |
| Lung ca. NCI-H23 | 5.8 | Brain (fetal) | 25.7 |
| Lung ca. NCI-H460 | 10.3 | Brain (Hippocampus) Pool | 42.9 |
| Lung ca. HOP-62 | 7.0 | Cerebral Cortex Pool | 100.0 |
| Lung ca. NCI-H522 | 2.9 | Brain (Substantia nigra) Pool | 76.3 |
| Liver | 0.1 | Brain (Thalamus) Pool | 63.7 |
| Fetal Liver | 1.3 | Brain (whole) | 56.6 |
| Liver ca. HepG2 | 1.4 | Spinal Cord Pool | 9.3 |
| Kidney Pool | 26.2 | Adrenal Gland | 16.2 |
| Fetal Kidney | 3.5 | Pituitary gland Pool | 16.4 |
| Renal ca. 786-0 | 26.4 | Salivary Gland | 13.4 |

Table SD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3317, Run 164683049 | Tissue Name | Rel. Exp.(%) Ag3317, Run 164683049 |
|--------------------------------|--|---|--|
| Secondary Th1 act | 21.6 | HUVEC IL-1beta | 3.8 |
| Secondary Th2 act | 23.2 | HUVEC IFN gamma | 12.5 |
| Secondary Tr1 act | 22.8 | HUVEC TNF alpha + IFN gamma | 2.9 |
| Secondary Th1 rest | 12.7 | HUVEC TNF alpha + IL4 | 9.0 |
| Secondary Th2 rest | 9.3 | HUVEC IL-11 | 4.0 |
| Secondary Tr1 rest | 33.7 | Lung Microvascular EC none | 24.3 |
| Primary Th1 act | 44.1 | Lung Microvascular EC TNFalpha + IL-1beta | 11.3 |
| Primary Th2 act | 49.3 | Microvascular Dermal EC none | 41.5 |
| Primary Tr1 act | 74.2 | Microvasular Dermal EC TNFalpha + IL-1beta | 17.2 |
| Primary Th1 rest | 38.2 | Bronchial epithelium TNFalpha + IL1beta | 31.2 |
| Primary Th2 rest | 44.4 | Small airway epithelium none | 8.0 |
| Primary Tr1 rest | 50.0 | Small airway epithelium TNFalpha + IL-1beta | 11.1 |
| CD45RA CD4 lymphocyte act | 41.2 | Coronery artery SMC rest | 20.6 |
| CD45RO CD4 lymphocyte act | 25.0 | Coronery artery SMC TNFalpha + IL-1beta | 19.6 |
| CD8 lymphocyte act | 17.8 | Astrocytes rest | 14.7 |
| Secondary CD8 lymphocyte rest | 21.8 | Astrocytes TNFalpha + IL-1beta | 11.0 |
| Secondary CD8 lymphocyte act | 7.4 | KU-812 (Basophil) rest | 2.1 |
| CD4 lymphocyte none | 21.8 | KU-812 (Basophil) PMA/ionomycin | 12.9 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 5.8 | CCD1106 (Keratinocytes) none | 30.6 |
| LAK cells rest | 51.1 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 23.7 |
| LAK cells IL-2 | 7.0 | Liver cirrhosis | 0.8 |

| gamma | gamma | gamma | gamma |
|-----------------------|-------|---------------|-------|
| LAK cells IL-2+ IL-18 | 28.7 | NCI-H292 IL-4 | 43.5 |

| | | | |
|-------------------------------|------|---------------------------------------|-------|
| LAK cells PMA/ionomycin | 20.6 | NCI-H292 IL-9 | 36.3 |
| NK Cells IL-2 rest | 13.5 | NCI-H292 IL-13 | 35.6 |
| Two Way MLR 3 day | 33.0 | NCI-H292 IFN gamma | 24.3 |
| Two Way MLR 5 day | 9.6 | HPAEC none | 22.8 |
| Two Way MLR 7 day | 10.0 | HPAEC TNF alpha + IL-1 beta | 8.3 |
| PBMC rest | 12.0 | Lung fibroblast none | 11.8 |
| PBMC PWM | 24.7 | Lung fibroblast TNF alpha + IL-1 beta | 1.2 |
| PBMC PHA-L | 32.5 | Lung fibroblast IL-4 | 19.2 |
| Ramos (B cell) none | 1.5 | Lung fibroblast IL-9 | 12.1 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 14.8 |
| B lymphocytes PWM | 41.2 | Lung fibroblast IFN gamma | 17.2 |
| B lymphocytes CD40L and IL-4 | 14.5 | Dermal fibroblast CCD1070 rest | 100.0 |
| EOL-1 dbcAMP | 20.0 | Dermal fibroblast CCD1070 TNF alpha | 57.8 |
| EOL-1 dbcAMP PMA/ionomycin | 60.3 | Dermal fibroblast CCD1070 IL-1 beta | 14.2 |
| Dendritic cells none | 55.5 | Dermal fibroblast IFN gamma | 24.1 |
| Dendritic cells LPS | 26.1 | Dermal fibroblast IL-4 | 39.0 |
| Dendritic cells anti-CD40 | 74.7 | IBD Colitis 2 | 1.6 |
| Monocytes rest | 48.0 | IBD Crohn's | 2.7 |
| Monocytes LPS | 15.4 | Colon | 19.1 |
| Macrophages rest | 98.6 | Lung | 14.4 |
| Macrophages LPS | 5.6 | Thymus | 10.5 |
| HUVEC none | 27.9 | Kidney | 100.0 |
| HUVEC starved | 27.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3317 - This panel does not show differential expression of this gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.4 for discussion of utility of this gene in the central nervous system.

throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, and

cerebral cortex. Highest expression is observed in the cerebral cortex (CT=29.0). This gene encodes a calmodulin-dependent protein kinase IV homolog, which is known to play a role in Ca²⁺ signaling in the CNS that controls neuronal growth, differentiation, and plasticity. Mice deficient in calmodulin-dependent protein kinase IV were found to have cerebellar defects. Therefore, this gene may play a role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Based on expression in this panel, this gene may be also be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

References:

1. Okuno S, Kitani T, Fujisawa H. Evidence for the existence of Ca²⁺/calmodulin-dependent protein kinase IV kinase isoforms in rat brain. *J Biochem (Tokyo)* 1996 Jun;119(6):1176-81.
2. Ribar TJ, Rodriguez RM, Khiroug L, Wetsel WC, Augustine GJ, Means AR. Cerebellar defects in Ca²⁺/calmodulin kinase IV-deficient mice. *J Neurosci* 2000 Nov 15;20(22):RC107.

Panel 4D Summary: Ag3317 - This gene was found to have low expression across almost all the samples on this panel, with the highest level of expression seen in kidney and resting dermal fibroblasts (CTs=32). Expression of Ca²⁺/calmodulin-dependent kinase type IV in thymocytes has been found in mice, where it plays a role in Ca²⁺-dependent gene transcription.

1. Raman V, Blaeser F, Ho N, Engle DL, Williams CB, Chatila TA. Requirement for Ca²⁺/calmodulin-dependent kinase type IV/Gr in setting the thymocyte selection threshold. *J Immunol* 2001 Dec 1;167(11):6270-8.

T. CG57709-01: Novel mitochondrial protein

Expression of gene CG57709-01 was assessed using the primer-probe set Ag3323, described in Table TA. Results of the RTQ-PCR runs are shown in Tables TB, TC and TD.

Table TA. Probe Name Ag3323

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-atgtgcagaggatacgcatg-3' | 20 | 589 | 450 |
| Probe | TET-5'-tgcaaaacaggaqaqacaqqqqqq-3' - TAMRA | 26 | 626 | 451 |
| Reverse | 5'-tggttctggcattctagacg-3' | 20 | 665 | 452 |

Table TB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3323, Run 210144152 | Tissue Name | Rel. Exp.(%) Ag3323, Run 210144152 |
|------------------------|------------------------------------|-------------------------------|------------------------------------|
| AD 1 Hippo | 22.5 | Control (Path) 3 Temporal Ctx | 5.2 |
| AD 2 Hippo | 29.5 | Control (Path) 4 Temporal Ctx | 32.5 |
| AD 3 Hippo | 6.9 | AD 1 Occipital Ctx | 18.6 |
| AD 4 Hippo | 7.4 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 hippo | 82.4 | AD 3 Occipital Ctx | 7.6 |
| AD 6 Hippo | 66.4 | AD 4 Occipital Ctx | 17.8 |
| Control 2 Hippo | 27.5 | AD 5 Occipital Ctx | 30.8 |
| Control 4 Hippo | 11.9 | AD 6 Occipital Ctx | 48.6 |
| Control (Path) 3 Hippo | 8.4 | Control 1 Occipital Ctx | 4.0 |
| AD 1 Temporal Ctx | 18.6 | Control 2 Occipital Ctx | 58.2 |
| AD 2 Temporal Ctx | 30.6 | Control 3 Occipital Ctx | 14.2 |

AD 1 → Temporal Ctx

Control (Path)
Occipital Ctx

| | | | |
|-------------------------------|-------|--------------------------------|------|
| AD 5 Inf Temporal Ctx | 100.0 | Control (Path) 2 Occipital Ctx | 12.6 |
| AD 5 Sup Temporal Ctx | 42.6 | Control (Path) 3 Occipital Ctx | 2.4 |
| AD 6 Inf Temporal Ctx | 48.6 | Control (Path) 4 Occipital Ctx | 14.6 |
| AD 6 Sup Temporal Ctx | 42.0 | Control 1 Parietal Ctx | 6.5 |
| Control 1 Temporal Ctx | 6.3 | Control 2 Parietal Ctx | 48.0 |
| Control 2 Temporal Ctx | 39.0 | Control 3 Parietal Ctx | 19.6 |
| Control 3 Temporal Ctx | 13.1 | Control (Path) 1 Parietal Ctx | 61.1 |
| Control 4 Temporal Ctx | 8.9 | Control (Path) 2 Parietal Ctx | 19.3 |
| Control (Path) 1 Temporal Ctx | 53.6 | Control (Path) 3 Parietal Ctx | 3.8 |
| Control (Path) 2 Temporal Ctx | 34.2 | Control (Path) 4 Parietal Ctx | 42.6 |

Table TC. Panel 1.3D

| Tissue Name | Rel. Exp.(%) Ag3323, Run 165678151 | Tissue Name | Rel. Exp.(%) Ag3323, Run 165678151 |
|--------------------------|------------------------------------|-------------------------------|------------------------------------|
| Liver adenocarcinoma | 25.0 | Kidney (fetal) | 6.5 |
| Pancreas | 12.8 | Renal ca. 786-0 | 14.3 |
| Pancreatic ca. CAPAN 2 | 24.5 | Renal ca. A498 | 34.2 |
| Adrenal gland | 12.2 | Renal ca. RXF 393 | 14.2 |
| Thyroid | 6.9 | Renal ca. ACHN | 12.9 |
| Salivary gland | 14.0 | Renal ca. UO-31 | 48.6 |
| Pituitary gland | 10.1 | Renal ca. TK-10 | 7.2 |
| Brain (fetal) | 13.7 | Liver | 20.2 |
| Brain (whole) | 29.7 | Liver (fetal) | 22.1 |
| Brain (amygdala) | 21.3 | Liver ca. (hepatoblast) HepG2 | 21.3 |
| Brain (cerebellum) | 24.7 | Lung | 6.7 |
| Brain (hippocampus) | 25.7 | Lung (fetal) | 14.8 |
| Brain (substantia nigra) | 20.0 | Lung ca. (small cell) | 39.8 |

| | | | |
|-----------------|------|----------------------------|------|
| Cerebral Cortex | 53.3 | Lung ca. (small cell var.) | 42.3 |
|-----------------|------|----------------------------|------|

| | | | |
|-----------------------------|-------|--------------------------------|------|
| | | SHP-77 | |
| Spinal cord | 16.5 | Lung ca. (large cell)NCI-H460 | 25.7 |
| glio/astro U87-MG | 8.9 | Lung ca. (non-sm. cell) A549 | 12.0 |
| glio/astro U-118-MG | 100.0 | Lung ca. (non-s.cell) NCI-H23 | 9.1 |
| astrocytoma SW1783 | 14.6 | Lung ca. (non-s.cell) HOP-62 | 9.5 |
| neuro*; met SK-N-AS | 43.2 | Lung ca. (non-s.cl) NCI-H522 | 10.7 |
| astrocytoma SF-539 | 13.9 | Lung ca. (squam.) SW 900 | 12.4 |
| astrocytoma SNB-75 | 29.7 | Lung ca. (squam.) NCI-H596 | 59.0 |
| glioma SNB-19 | 13.5 | Mammary gland | 10.6 |
| glioma U251 | 43.8 | Breast ca.* (pl.ef) MCF-7 | 46.3 |
| glioma SF-295 | 17.7 | Breast ca.* (pl.ef) MDA-MB-231 | 31.6 |
| Heart (fetal) | 22.7 | Breast ca.* (pl.ef) T47D | 15.1 |
| Heart | 14.5 | Breast ca. BT-549 | 54.0 |
| Skeletal muscle (fetal) | 6.8 | Breast ca. MDA-N | 11.5 |
| Skeletal muscle | 55.5 | Ovary | 8.7 |
| Bone marrow | 10.7 | Ovarian ca. OVCAR-3 | 26.2 |
| Thymus | 5.5 | Ovarian ca. OVCAR-4 | 21.6 |
| Spleen | 13.3 | Ovarian ca. OVCAR-5 | 20.9 |
| Lymph node | 24.8 | Ovarian ca. OVCAR-8 | 12.6 |
| Colorectal | 8.8 | Ovarian ca. IGROV-1 | 4.4 |
| Stomach | 15.1 | Ovarian ca.* (ascites) SK-OV-3 | 23.5 |
| Small intestine | 28.3 | Uterus | 14.3 |
| Colon ca. SW480 | 27.5 | Placenta | 6.9 |
| Colon ca.* SW620(SW480 met) | 17.6 | Prostate | 9.5 |

| | | | |
|-------------------|------|----------|-----|
| Colon ca. TiCL-17 | 12.2 | Testis | |
| Colon ca. CaCo-2 | 12.7 | Melanoma | 7.6 |

| | | | |
|-------------------------------------|------|-------------------------------|------|
| | | Hs688(A).T | |
| Colon ca. tissue(ODO3866) | 22.5 | Melanoma* (met) Hs688(B).T | 6.6 |
| Colon ca. HCC-2998 | 25.2 | Melanoma UACC-62 | 19.6 |
| Gastric ca.* (liver met) NCI-N87 | 29.5 | Melanoma M14 | 39.2 |
| Bladder | 6.1 | Melanoma LOX IMVI | 13.4 |
| Trachea | 13.2 | Melanoma* (met) SK-MEL-5 | 21.2 |
| Kidney | 15.6 | Adipose | 6.5 |

Table TD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3323, Run 165296416 | Tissue Name | Rel. Exp.(%) Ag3323, Run 165296416 |
|------------------------------|--|--|--|
| Secondary Th1 act | 32.3 | HUVEC IL-1beta | 3.8 |
| Secondary Th2 act | 22.8 | HUVEC IFN gamma | 12.0 |
| Secondary Tr1 act | 29.9 | HUVEC TNF alpha + IFN gamma | 8.1 |
| Secondary Th1 rest | 3.8 | HUVEC TNF alpha + IL4 | 11.1 |
| Secondary Th2 rest | 4.3 | HUVEC IL-11 | 8.4 |
| Secondary Tr1 rest | 6.0 | Lung Microvascular EC none | 7.6 |
| Primary Th1 act | 33.0 | Lung Microvascular EC TNFalpha + IL-1beta | 6.9 |
| Primary Th2 act | 25.0 | Microvascular Dermal EC none | 14.7 |
| Primary Tr1 act | 40.1 | Microvasular Dermal EC TNFalpha + IL-1beta | 7.6 |
| Primary Th1 rest | 17.8 | Bronchial epithelium TNFalpha + IL-1beta | 17.3 |
| Primary Th2 rest | 11.6 | Small airway epithelium none | 6.6 |
| Primary Tr1 rest | 15.0 | Small airway epithelium TNFalpha + IL-1beta | 18.4 |
| CD45RA CD4 lymphocyte act | 15.0 | Coronery artery SMC rest | 9.9 |
| CD45RO CD4 lymphocyte act | 24.7 | Coronery artery SMC TNFalpha + IL-1beta | 6.5 |

| | | | |
|-----------------|------|------------------------|------|
| lymphocyte rest | | IL-1beta | |
| Secondary CD8 | 12.9 | KU-812 (Basophil) rest | 14.0 |

| | | | |
|------------------------------------|-------|--|------|
| lymphocyte act | | | |
| CD4 lymphocyte none | 2.9 | KU-812 (Basophil) PMA/ionomycin | 22.1 |
| 2ry Th1/Th2/Tr1_anti- CD95 CH11 | 5.4 | CCD1106 (Keratinocytes) none | 16.0 |
| LAK cells rest | 7.2 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 8.1 |
| LAK cells IL-2 | 17.2 | Liver cirrhosis | 1.7 |
| LAK cells IL-2+IL-12 | 15.1 | Lupus kidney | 1.0 |
| LAK cells IL-2+IFN gamma | 27.9 | NCI-H292 none | 30.1 |
| LAK cells IL-2+ IL-18 | 17.7 | NCI-H292 IL-4 | 49.0 |
| LAK cells PMA/ionomycin | 1.9 | NCI-H292 IL-9 | 33.2 |
| NK Cells IL-2 rest | 8.4 | NCI-H292 IL-13 | 26.2 |
| Two Way MLR 3 day | 9.9 | NCI-H292 IFN gamma | 26.6 |
| Two Way MLR 5 day | 18.4 | HPAEC none | 11.7 |
| Two Way MLR 7 day | 8.9 | HPAEC TNF alpha + IL-1 beta | 7.5 |
| PBMC rest | 3.8 | Lung fibroblast none | 8.0 |
| PBMC PWM | 50.3 | Lung fibroblast TNF alpha + IL-1 beta | 5.5 |
| PBMC PHA-L | 29.3 | Lung fibroblast IL-4 | 19.1 |
| Ramos (B cell) none | 33.9 | Lung fibroblast IL-9 | 15.3 |
| Ramos (B cell) ionomycin | 83.5 | Lung fibroblast IL-13 | 11.4 |
| B lymphocytes PWM | 100.0 | Lung fibroblast IFN gamma | 16.5 |
| B lymphocytes CD40L and IL-4 | 22.4 | Dermal fibroblast CCD1070 rest | 28.9 |
| EOL-1 dbcAMP | 10.5 | Dermal fibroblast CCD1070 TNF alpha | 31.2 |
| EOL-1 dbcAMP PMA/ionomycin | 3.7 | Dermal fibroblast CCD1070 IL-1 beta | 11.3 |
| Dendritic cells none | 9.9 | Dermal fibroblast IFN gamma | 5.2 |
| Dendritic cells LPS | 6.3 | Dermal fibroblast IL-4 | 12.3 |
| Dendritic cells anti- CD40 | 7.3 | IBD Colitis 2 | 0.7 |
| Monocytes rest | 7.0 | IBD Crohn's | 1.0 |

| Macrophages LPS | | Environs | |
|-----------------|------|----------|------|
| HUVEC none | 11.9 | Kidney | 12.3 |

| | | | |
|---------------|------|--|--|
| HUVEC starved | 24.8 | | |
|---------------|------|--|--|

CNS_neurodegeneration_v1.0 Summary: Ag3323 This panel does not show differential expression of the CG57709-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

Panel 1.3D Summary: Ag3323 - This gene is expressed at moderate levels in all samples on this panel, with highest expression in a brain cancer cell line. Expression is also seen in all the cancer cell lines on this panel. Thus, expression of this gene could be used to differentiate between this brain cancer cell line sample and other samples on this panel and as a marker for brain cancer.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that deregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This molecule is also expressed at moderate to low levels in the CNS and may be a small molecule target for the treatment of neurologic diseases such as Alzheimer's disease, Parkinson's disease, epilepsy, schizophrenia, stroke and multiple sclerosis.

Panel 4D Summary: Ag3323 - This gene is expressed at high to moderate levels in all samples on this panel, with highest expression in B lymphocytes stimulated with pokeweed mitogen (CT=24.5). In addition, this gene is expressed at higher levels in ionomycin-activated Ramos B lymphocytes. The high levels of expression in activated B lymphocytes suggests that therapies that antagonize the function of this gene product may reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

5-(CH₂)₇HYDROXY-3,5-DIMETHYLHEPTANOIC ACID (GLYOXALASE II)

Expression of gene CG57700-01 was assessed using the primer-probe set Ag3311, described in Table UA. Results of the RTQ-PCR runs are shown in Table UB.

Table UA. Probe Name Ag3311

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' - acgcttagcaacctggagtt - 3' | 20 | 536 | 453 |
| Probe | TET-5' - accacgtgagagccaagctgtcct - 3' TAMRA | 24 | 582 | 454 |
| Reverse | 5' - gtcatccatccctttctg - 3' | 21 | 611 | 456 |

Table UB. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3311, Run 164682845 | Tissue Name | Rel. Exp.(%) Ag3311, Run 164682845 |
|-------------------------------|--|---|--|
| Secondary Th1 act | 10.2 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 3.8 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 0.0 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 0.0 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 0.0 |
| Primary Tr1 act | 1.6 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 5.1 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 0.0 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 0.0 | Coronery artery SMC rest | 0.0 |
| CD45RO CD4 | 0.0 | Coronery artery SMC | 0.0 |
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 0.0 |

| | | | |
|--------------------------------|-----|--|------|
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.0 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 4.2 |
| LAK cells rest | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 2.7 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 0.0 |
| LAK cells IL-2+IL-12 | 0.0 | Lupus kidney | 0.0 |
| LAK cells IL-2+IFN gamma | 0.0 | NCI-H292 none | 0.0 |
| LAK cells IL-2+ IL-18 | 0.0 | NCI-H292 IL-4 | 0.0 |
| LAK cells PMA/ionomycin | 0.0 | NCI-H292 IL-9 | 0.0 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 0.0 |
| Two Way MLR 3 day | 4.5 | NCI-H292 IFN gamma | 1.9 |
| Two Way MLR 5 day | 0.0 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 0.0 |
| PBMC PWM | 3.7 | Lung fibroblast TNF alpha + IL-1 beta | 0.0 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 14.1 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 4.3 |
| B lymphocytes PWM | 0.0 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 rest | 0.0 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 |
| EOL-1 dbcAMP PMA/ionomycin | 1.6 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 2.1 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 0.0 | Dermal fibroblast IL-4 | 3.0 |
| Dendritic cells anti-CD40 | 2.5 | IBD Colitis 2 | 0.0 |

| | | | |
|------------------|-----|--------|-----|
| Macrophages rest | 0.0 | Thymus | 0.0 |
| Macrophages LPS | 0.0 | | |

| | | | |
|---------------|-----|--------|-----|
| HUVEC none | 0.0 | Kidney | 2.4 |
| HUVEC starved | 0.0 | | |

AI_comprehensive panel_v1.0 Summary: Ag3311 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CNS_neurodegeneration_v1.0 Summary: Ag3311 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3311 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3311 - Significant expression of this gene is seen only in colon (CT=33.9). Therefore, expression of this gene can be used to distinguish between this sample and the others on the panel and between healthy and inflammed bowel. Since expression is not detectable in samples derived from Crohn's and colitis patients, therapeutic modulation of the expression or function of this gene may be useful in the treatment of inflammatory bowel disease.

V. CG58553-01: vasopressin receptor

Expression of gene CG58553-01 was assessed using the primer-probe set Ag3372, described in Table VA. Results of the RTQ-PCR runs are shown in Tables VB and VC.

Table VA. Probe Name Ag3372

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -cgatatctggtcatcacaca 3' | 19 | 1983 | 457 |
| Probe | TET-5' -ccacccacaacacctcccaaggaact-3' - TAMRA | 24 | 2017 | 458 |
| Reverse | 5' -agcctcagaaggtcgagatg-3' | 20 | 2041 | 459 |

Table VB. Panel 1.3D

| Tissue Name | Rel. Exp.(%) Ag3372, Run 165524269 | Tissue Name | Rel. Exp.(%) Ag3372, Run 165524269 |
|----------------------|---------------------------------------|----------------|---------------------------------------|
| Pancreatic ca. CAPAN | 0.0 | Renal ca. A498 | 0.1 |

| | | | |
|--------------------------|-----|-----------------------------------|-----|
| 2 | | | |
| Adrenal gland | 0.0 | Renal ca. RXF 393 | 0.0 |
| Thyroid | 0.1 | Renal ca. ACHN | 0.0 |
| Salivary gland | 0.1 | Renal ca. UO-31 | 0.0 |
| Pituitary gland | 0.2 | Renal ca. TK-10 | 0.0 |
| Brain (fetal) | 0.0 | Liver | 2.1 |
| Brain (whole) | 0.3 | Liver (fetal) | 0.0 |
| Brain (amygdala) | 0.0 | Liver ca. (hepatoblast) HepG2 | 0.2 |
| Brain (cerebellum) | 0.1 | Lung | 2.4 |
| Brain (hippocampus) | 0.5 | Lung (fetal) | 0.2 |
| Brain (substantia nigra) | 0.2 | Lung ca. (small cell) LX-1 | 0.0 |
| Brain (thalamus) | 0.0 | Lung ca. (small cell) NCI-H69 | 0.0 |
| Cerebral Cortex | 0.0 | Lung ca. (s.cell var.) SHP-77 | 0.1 |
| Spinal cord | 1.0 | Lung ca. (large cell)NCI-H460 | 0.0 |
| glio/astro U87-MG | 0.0 | Lung ca. (non-sm. cell) A549 | 0.1 |
| glio/astro U-118-MG | 0.0 | Lung ca. (non-s.cell) NCI-H23 | 0.6 |
| astrocytoma SW1783 | 0.0 | Lung ca. (non-s.cell) HOP-62 | 0.1 |
| neuro*; met SK-N-AS | 0.0 | Lung ca. (non-s.cl) NCI-H522 | 0.0 |
| astrocytoma SF-539 | 0.0 | Lung ca. (squam.) SW 900 | 0.0 |
| astrocytoma SNB-75 | 0.1 | Lung ca. (squam.) NCI-H596 | 0.0 |
| glioma SNB-19 | 0.4 | Mammary gland | 0.7 |
| glioma U251 | 0.2 | Breast ca.* (pl.ef) MCF-7 | 0.0 |
| glioma SF-295 | 0.0 | Breast ca.* (pl.ef) MDA-MB-231 | 0.0 |
| Heart (fetal) | 0.0 | Breast ca.* (pl.ef) T47D | 0.1 |
| Heart | 0.0 | Breast ca. BT-549 | 0.0 |
| Skeletal muscle (fetal) | 0.0 | Breast ca. MDA-N | 0.0 |

| | | | |
|--------|----|--------------------|-----|
| Thymus | 1. | Ovarian ca. OVCAR- | 0.0 |
|--------|----|--------------------|-----|

| | | | |
|-------------------------------------|--------------|-----------------------------------|-----|
| | | 4 | |
| Spleen | 2.8 | Ovarian ca. OVCAR-5 | 0.2 |
| Lymph node | 5.5 | Ovarian ca. OVCAR-8 | 0.2 |
| Colorectal | 0.2 | Ovarian ca. IGROV-1 | 0.0 |
| Stomach | 1.2 | Ovarian ca.* (ascites) SK-OV-3 | 0.0 |
| Small intestine | 100.0 | Uterus | 0.0 |
| Colon ca. SW480 | 0.0 | Placenta | 0.8 |
| Colon ca.* SW620(SW480 met) | 0.0 | Prostate | 0.1 |
| Colon ca. HT29 | 0.0 | Prostate ca.* (bone met)PC-3 | 0.0 |
| Colon ca. HCT-116 | 0.0 | Testis | 1.4 |
| Colon ca. CaCo-2 | 0.3 | Melanoma Hs688(A).T | 0.0 |
| Colon ca. tissue(ODO3866) | 0.7 | Melanoma* (met) Hs688(B).T | 0.0 |
| Colon ca. HCC-2998 | 3.8 | Melanoma UACC-62 | 0.0 |
| Gastric ca.* (liver met) NCI-N87 | 1.0 | Melanoma M14 | 0.2 |
| Bladder | 0.0 | Melanoma LOX IMVI | 0.2 |
| Trachea | 0.1 | Melanoma* (mct) SK-MEL-5 | 0.4 |
| Kidney | 0.6 | Adipose | 1.3 |

Table VC. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3372, Run 165296616 | Tissue Name | Rel. Exp.(%) Ag3372, Run 165296616 |
|--------------------|---|--------------------------------|---|
| Secondary Th1 act | 1.4 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 1.4 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 2.9 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 5.4 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 6.4 | HUVEC IL-11 | 0.0 |

Primary Th1 act

IFN-gamma + IL-1beta

| | | | |
|--------------------------------|------|--|-----|
| Primary Th2 act | 18.9 | Microvascular Dermal EC none | 0.0 |
| Primary Tr1 act | 27.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 27.5 | Bronchial epithelium TNFalpha + IL1beta | 0.1 |
| Primary Th2 rest | 13.6 | Small airway epithelium none | 0.0 |
| Primary Tr1 rest | 32.8 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 3.0 | Coronery artery SMC rest | 0.0 |
| CD45RO CD4 lymphocyte act | 8.5 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 5.8 | Astrocytes rest | 0.0 |
| Secondary CD8 lymphocyte rest | 3.1 | Astrocytes TNFalpha + IL-1beta | 0.0 |
| Secondary CD8 lymphocyte act | 2.9 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 4.7 | KU-812 (Basophil) PMA/ionomycin | 0.1 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 7.5 | CCD1106 (Keratinocytes) none | 0.0 |
| LAK cells rest | 1.8 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |
| LAK cells IL-2 | 5.8 | Liver cirrhosis | 1.5 |
| LAK cells IL-2+IL-12 | 2.3 | Lupus kidney | 0.6 |
| LAK cells IL-2+IFN gamma | 5.5 | NCI-H292 none | 2.5 |
| LAK cells IL-2+ IL-18 | 5.5 | NCI-H292 IL-4 | 1.8 |
| LAK cells PMA/ionomycin | 2.7 | NCI-H292 IL-9 | 5.9 |
| NK Cells IL-2 rest | 6.0 | NCI-H292 IL-13 | 2.3 |
| Two Way MLR 3 day | 2.1 | NCI-H292 IFN gamma | 3.0 |
| Two Way MLR 5 day | 0.9 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 1.8 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 1.5 | Lung fibroblast none | 0.0 |
| PBMC PWM | 5.6 | Lung fibroblast TNF alpha + IL-1 beta | 0.0 |
| PBMC PHA L | 0.0 | Lung fibroblast IL-4 | 0.0 |

| NAME (LYMPH) | Conc (uM) | Conc (uM) | Conc (uM) |
|-------------------|-----------|---------------------|-----------|
| ionomycin | | Lung fibroblast | |
| B lymphocytes PWM | 2.2 | Lung fibroblast IFN | 0.0 |

| | | | |
|------------------------------|-----|-------------------------------------|--------------|
| | | gamma | |
| B lymphocytes CD40L and IL-4 | 3.7 | Dermal fibroblast CCD1070 rest | 0.0 |
| EOL-1 dbcAMP | 1.0 | Dermal fibroblast CCD1070 TNF alpha | 5.2 |
| EOL-1 dbcAMP PMA/ionomycin | 0.4 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 0.2 | Dermal fibroblast IFN gamma | 0.1 |
| Dendritic cells LPS | 0.0 | Dermal fibroblast IL-4 | 0.0 |
| Dendritic cells anti-CD40 | 0.0 | IBD Colitis 2 | 0.4 |
| Monocytes rest | 0.3 | IBD Crohn's | 8.4 |
| Monocytes LPS | 0.2 | Colon | 100.0 |
| Macrophages rest | 0.7 | Lung | 0.9 |
| Macrophages LPS | 0.0 | Thymus | 8.1 |
| HUVEC none | 0.0 | Kidney | 6.8 |
| HUVEC starved | 0.0 | | |

Panel 1.3D Summary: Ag3372 Highest expression of the CG58553-01 gene is seen in the small intestine sample (CT=26.8). This gene encodes a novel vasopressin gene that plays a role in regulating electrolyte transport in the colon. Therefore, regulation of the transcript or the protein it encodes could be important in maintaining normal cellular homeostasis and in the treatment of Crohn's disease and ulcerative colitis.

Among tissues with metabolic function, this gene is expressed in liver and adipose. Thus, this gene product may be involved in disorders that affect these tissues, such as obesity and type II diabetes.

Low, but significant expression is also seen in the hippocampus. The hippocampus is critical for learning and memory. Thus, this gene product may have utility treating CNS disorders involving memory deficits, including Alzheimer's disease and aging.

References:

- Sato Y, Hanai H, Nogaki A, Hirasawa K, Kaneko E, Hayashi H, Suzuki Y. Role of CG58553-01 in regulating the synthesis and release of the antidiuretic hormone in the mouse pituitary. *J Neurosci Res* 2002;60:101-106.

Panel 4D Summary: Ag3372 In agreement with the results seen in panel 1.4, the highest level of expression of this gene is in the colon sample (CT=27.5). Interestingly, the expression is significantly lower in the IBD colitis 2 (CT>35) and IBD Crohn's (CT=30.9)samples. Therefore, alterations in the expression of this gene may be used in the treatment of Crohn's disease and ulcerative colitis.

In addition, the expression of the CG58553-01 gene in several preparations of T lymphocytes suggests that small molecule antagonists, therapeutic antibodies specific for this molecule, or the extracellular domain of this protein, may be useful to reduce or eliminate the symptoms of Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, or psoriasis.

W. CG58626-01: Phospholipase

Expression of gene CG58626-01 was assessed using the primer-probe set Ag3386, described in Table WA. Results of the RTQ-PCR runs are shown in Tables WB, WC and WD.

Table WA. Probe Name Ag3386

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-agtggcggtcaaaacttactct-3' | 22 | 1386 | 460 |
| Probe | TET-5'-tggagacactgttgattccattactcctg-3' - TAMRA | 29 | 1411 | 461 |
| Reverse | 5'-ctgctgttcagcatatccctta-3' | 22 | 1455 | 462 |

Table WB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3386, Run 210154893 | Tissue Name | Rel. Exp.(%) Ag3386, Run 210154893 |
|-------------|------------------------------------|-------------------------------|------------------------------------|
| AD 1 Hippo | 6.4 | Control (Path) 3 Temporal Ctx | 4.2 |
| AD 2 Hippo | 21.5 | Control (Path) 4 Temporal Ctx | 25.0 |
| AD 3 Hippo | 5.0 | AD 1 Occipital Ctx | 14.4 |
| | | AD 2 Occipital Ctx | |

| | | | |
|-----------------|------|--------------------|------|
| AD 6 Hippo | | AD 4 Occipital Ctx | |
| Control 2 Hippo | 26.4 | AD 5 Occipital Ctx | 28.7 |

| | | | |
|-------------------------------|------|--------------------------------|-------|
| Control 4 Hippo | 4.5 | AD 6 Occipital Ctx | 52.5 |
| Control (Path) 3 Hippo | 4.0 | Control 1 Occipital Ctx | 2.4 |
| AD 1 Temporal Ctx | 13.5 | Control 2 Occipital Ctx | 56.3 |
| AD 2 Temporal Ctx | 24.5 | Control 3 Occipital Ctx | 11.0 |
| AD 3 Temporal Ctx | 3.8 | Control 4 Occipital Ctx | 4.3 |
| AD 4 Temporal Ctx | 18.9 | Control (Path) 1 Occipital Ctx | 100.0 |
| AD 5 Inf Temporal Ctx | 95.9 | Control (Path) 2 Occipital Ctx | 8.8 |
| AD 5 SupTemporal Ctx | 37.6 | Control (Path) 3 Occipital Ctx | 1.7 |
| AD 6 Inf Temporal Ctx | 52.5 | Control (Path) 4 Occipital Ctx | 12.3 |
| AD 6 Sup Temporal Ctx | 63.7 | Control 1 Parietal Ctx | 5.4 |
| Control 1 Temporal Ctx | 4.9 | Control 2 Parietal Ctx | 39.5 |
| Control 2 Temporal Ctx | 38.4 | Control 3 Parietal Ctx | 11.3 |
| Control 3 Temporal Ctx | 12.2 | Control (Path) 1 Parietal Ctx | 77.4 |
| Control 4 Temporal Ctx | 5.0 | Control (Path) 2 Parietal Ctx | 20.7 |
| Control (Path) 1 Temporal Ctx | 76.8 | Control (Path) 3 Parietal Ctx | 2.7 |
| Control (Path) 2 Temporal Ctx | 37.6 | Control (Path) 4 Parietal Ctx | 45.4 |

Table WC_General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3386, Run 217043839 | Tissue Name | Rel. Exp.(%) Ag3386, Run 217043839 |
|----------------------|------------------------------------|----------------------------------|------------------------------------|
| Adipose | 12.2 | Renal ca. TK-10 | 10.7 |
| Melanoma* Hs688(A).T | 26.4 | Bladder | 18.4 |
| Melanoma* Hs688(B).T | 30.4 | Gastric ca. (liver met.) NCI-N87 | 26.6 |

| | | |
|---------------|-----------------|------|
| ONCOLOGY | Colon ca. SW480 | 40.9 |
| Melanoma* SK- | 22.7 | |

| | | | |
|-------------------------------|------|-------------------------------------|-------|
| MEL-5 | | | |
| Squamous cell carcinoma SCC-4 | 11.2 | Colon ca.* (SW480 met) SW620 | 20.4 |
| Testis Pool | 47.0 | Colon ca. HT29 | 5.2 |
| Prostate ca.* (bone met) PC-3 | 80.1 | Colon ca. HCT-116 | 100.0 |
| Prostate Pool | 7.1 | Colon ca. CaCo-2 | 13.8 |
| Placenta | 3.2 | Colon cancer tissue | 13.6 |
| Uterus Pool | 6.4 | Colon ca. SW1116 | 10.2 |
| Ovarian ca. OVCAR-3 | 22.8 | Colon ca. Colo-205 | 1.8 |
| Ovarian ca. SK-OV-3 | 94.0 | Colon ca. SW-48 | 2.4 |
| Ovarian ca. OVCAR-4 | 4.7 | Colon Pool | 27.7 |
| Ovarian ca. OVCAR-5 | 29.3 | Small Intestine Pool | 14.6 |
| Ovarian ca. IGROV-1 | 12.7 | Stomach Pool | 12.2 |
| Ovarian ca. OVCAR-8 | 11.1 | Bone Marrow Pool | 6.9 |
| Ovary | 11.6 | Fetal Heart | 8.1 |
| Breast ca. MCF-7 | 36.9 | Heart Pool | 6.3 |
| Breast ca. MDA-MB-231 | 39.5 | Lymph Node Pool | 13.9 |
| Breast ca. BT 549 | 28.5 | Fetal Skeletal Muscle | 3.6 |
| Breast ca. T47D | 52.9 | Skeletal Muscle Pool | 6.7 |
| Breast ca. MDA-N | 11.3 | Spleen Pool | 17.1 |
| Breast Pool | 28.1 | Thymus Pool | 26.1 |
| Trachea | 11.0 | CNS cancer (glio/astro) U87-MG | 33.2 |
| Lung | 6.0 | CNS cancer (glio/astro) U-118-MG | 44.1 |
| Fetal Lung | 39.2 | CNS cancer (neuro;met) SK-N-AS | 44.4 |
| Lung ca. NCI-N417 | 6.3 | CNS cancer (astro) SF-539 | 10.4 |
| Lung ca. LX-1 | 33.9 | CNS cancer (astro) SNB-75 | 27.7 |
| Lung ca. NCI-H146 | 14.3 | CNS cancer (glio) SNB-75 | 10.2 |

| | | | |
|---------------|------|-----------------------|------|
| Lung ca. A549 | 25.3 | Brain (Amygdala) Pool | 23.2 |
|---------------|------|-----------------------|------|

| | | | |
|-------------------|------|-------------------------------|------|
| Lung ca. NCI-H526 | 5.8 | Brain (cerebellum) | 19.8 |
| Lung ca. NCI-H23 | 30.1 | Brain (fetal) | 35.6 |
| Lung ca. NCI-H460 | 20.2 | Brain (Hippocampus) Pool | 25.2 |
| Lung ca. HOP-62 | 11.9 | Cerebral Cortex Pool | 39.2 |
| Lung ca. NCI-H522 | 20.7 | Brain (Substantia nigra) Pool | 23.0 |
| Liver | 0.7 | Brain (Thalamus) Pool | 45.7 |
| Fetal Liver | 29.5 | Brain (whole) | 24.0 |
| Liver ca. HepG2 | 10.1 | Spinal Cord Pool | 22.5 |
| Kidney Pool | 21.3 | Adrenal Gland | 8.5 |
| Fetal Kidney | 19.5 | Pituitary gland Pool | 7.0 |
| Renal ca. 786-0 | 15.9 | Salivary Gland | 1.9 |
| Renal ca. A498 | 3.5 | Thyroid (female) | 3.2 |
| Renal ca. ACHN | 8.0 | Pancreatic ca. CAPAN2 | 3.7 |
| Renal ca. UO-31 | 12.2 | Pancreas Pool | 18.2 |

Table WD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3386, Run 165296474 | Tissue Name | Rel. Exp.(%) Ag3386, Run 165296474 |
|--------------------|--|--|--|
| Secondary Th1 act | 30.4 | HUVEC IL-1beta | 2.0 |
| Secondary Th2 act | 35.6 | HUVEC IFN gamma | 3.3 |
| Secondary Tr1 act | 27.9 | HUVEC TNF alpha + IFN gamma | 3.8 |
| Secondary Th1 rest | 8.9 | HUVEC TNF alpha + IL4 | 3.3 |
| Secondary Th2 rest | 8.0 | HUVEC IL-11 | 1.5 |
| Secondary Tr1 rest | 11.3 | Lung Microvascular EC none | 5.5 |
| Primary Th1 act | 57.4 | Lung Microvascular EC TNFalpha + IL-1beta | 4.8 |
| Primary Th2 act | 36.9 | Microvascular Dermal EC none | 3.7 |
| Primary Tr1 act | 51.1 | Microvasular Dermal EC TNFalpha + IL-1beta | 3.3 |
| Primary Th1 rest | 54.0 | Bronchial epithelium TNFalpha + IL1beta | 5.5 |
| Primary Th2 rest | 18.8 | Small airway epithelium none | 2.1 |

| | | | |
|---------------------------|------|--------------------------|-----|
| CD4SRA CD4 lymphocyte act | 12.4 | Coronery artery SMC rest | 4.6 |
|---------------------------|------|--------------------------|-----|

| | | | |
|--------------------------------|-------|---|------|
| CD45RO CD4 lymphocyte act | 33.9 | Coronery artery SMC TNFalpha + IL-1beta | 2.4 |
| CD8 lymphocyte act | 29.3 | Astrocytes rest | 3.0 |
| Secondary CD8 lymphocyte rest | 26.1 | Astrocytes TNFalpha + IL-1beta | 3.0 |
| Secondary CD8 lymphocyte act | 20.7 | KU-812 (Basophil) rest | 12.1 |
| CD4 lymphocyte none | 1.1 | KU-812 (Basophil) PMA/ionomycin | 27.7 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 12.8 | CCD1106 (Keratinocytes) none | 2.7 |
| LAK cells rest | 12.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.8 |
| LAK cells IL-2 | 24.3 | Liver cirrhosis | 0.3 |
| LAK cells IL-2+IL-12 | 28.7 | Lupus kidney | 0.7 |
| LAK cells IL-2+IFN gamma | 42.0 | NCI-H292 none | 8.1 |
| LAK cells IL-2+ IL-18 | 45.1 | NCI-H292 IL-4 | 9.5 |
| LAK cells PMA/ionomycin | 8.8 | NCI-H292 IL-9 | 8.5 |
| NK Cells IL-2 rest | 21.8 | NCI-H292 IL-13 | 4.5 |
| Two Way MLR 3 day | 18.7 | NCI-H292 IFN gamma | 3.6 |
| Two Way MLR 5 day | 11.0 | HPAEC none | 2.5 |
| Two Way MLR 7 day | 10.9 | HPAEC TNF alpha + IL-1 beta | 3.0 |
| PBMC rest | 4.5 | Lung fibroblast none | 4.6 |
| PBMC PWM | 66.0 | Lung fibroblast TNF alpha + IL-1 beta | 3.3 |
| PBMC PHA-L | 17.9 | Lung fibroblast IL-4 | 12.1 |
| Ramos (B cell) none | 26.1 | Lung fibroblast IL-9 | 12.3 |
| Ramos (B cell) ionomycin | 100.0 | Lung fibroblast IL-13 | 6.7 |
| B lymphocytes PWM | 88.9 | Lung fibroblast IFN gamma | 16.6 |
| B lymphocytes CD40L and IL-4 | 49.3 | Dermal fibroblast CCD1070 rest | 8.2 |
| EOL-1 dbcAMP | 13.0 | Dermal fibroblast CCD1070 TNF alpha | 37.1 |
| EOL-1 dbcAMP PMA/ionomycin | 9.5 | Dermal fibroblast CCD1070 IL-1 beta | 4.4 |
| | | Dermal fibroblast IFN | |

| | | | |
|---------------------------|-----|---------------|-----|
| Dendritic cells anti-CD40 | 4.5 | IBD Colitis 2 | 0.7 |
|---------------------------|-----|---------------|-----|

| | | | |
|------------------|-----|-------------|------|
| Monocytes rest | 4.7 | IBD Crohn's | 0.5 |
| Monocytes LPS | 2.6 | Colon | 3.4 |
| Macrophages rest | 8.8 | Lung | 4.9 |
| Macrophages LPS | 2.8 | Thymus | 4.1 |
| HUVEC none | 2.8 | Kidney | 13.0 |
| HUVEC starved | 6.4 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3386 This panel confirms the expression of this gene at moderate to low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3386 This gene is moderately expressed in most of the samples on this panel. Based on expression in this panel, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3386 The CG58626-01 transcript is expressed ubiquitously in this panel. Highest expression of this transcript is seen in activated Ramos cells and activated B cells (CTs=27). The expression of this transcript in activated lymphoid cells when compared to non-activated cells suggests that the CG58626-01 gene may be important for the diagnosis

activity of this gene product might important for the treatment of autoimmune disease, allergy, and delayed type hypersensitivity.

X. CG57597-01: Hypothetical protein

Expression of gene CG57597-01 was assessed using the primer-probe set Ag3293, described in Table XA.

Table XA. Probe Name Ag3293

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-cagaaaacctgtgaactctgcat-3' | 22 | 40 | 463 |
| Probe | TET-5'-atgcaccaccactcctggctaattt-3' - TAMRA | 26 | 69 | 464 |
| Reverse | 5'-ataaaaggtttgagccggatt-3' | 21 | 115 | 465 |

CNS_neurodegeneration_v1.0 Summary: Ag3293 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3293 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3293 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Y. CG57804-01: talin

Expression of gene CG57804-01 was assessed using the primer-probe set Ag3337, described in Table YA. Results of the RTQ-PCR runs are shown in Tables YB, YC and YD.

Table YA. Probe Name Ag3337

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-ggatttcaagcccagataacaat-3' | 22 | 781 | 466 |
| Probe | TET-5'-tggacacctatgtggAACATAACACA-3' - TAMRA | 26 | 804 | 467 |
| Reverse | 5'-ggcaggaatttccttcagatc-3' | 20 | 844 | 468 |

| Tissue Name | Rel. Exp.(%) Ag3337, | Tissue Name | Rel. Exp.(%) Ag3337, |
|-------------|----------------------|-------------|----------------------|
|-------------|----------------------|-------------|----------------------|

| | Run 210138775 | | Run 210138775 |
|----------------------------------|----------------------|-----------------------------------|----------------------|
| AD 1 Hippo | 6.8 | Control (Path) 3 Temporal Ctx | 3.6 |
| AD 2 Hippo | 25.3 | Control (Path) 4 Temporal Ctx | 22.4 |
| AD 3 Hippo | 3.6 | AD 1 Occipital Ctx | 5.6 |
| AD 4 Hippo | 5.7 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 Hippo | 78.5 | AD 3 Occipital Ctx | 2.2 |
| AD 6 Hippo | 27.5 | AD 4 Occipital Ctx | 14.7 |
| Control 2 Hippo | 27.4 | AD 5 Occipital Ctx | 44.1 |
| Control 4 Hippo | 8.1 | AD 6 Occipital Ctx | 16.6 |
| Control (Path) 3 Hippo | 4.3 | Control 1 Occipital Ctx | 1.6 |
| AD 1 Temporal Ctx | 7.6 | Control 2 Occipital Ctx | 67.8 |
| AD 2 Temporal Ctx | 24.5 | Control 3 Occipital Ctx | 11.9 |
| AD 3 Temporal Ctx | 3.3 | Control 4 Occipital Ctx | 3.0 |
| AD 4 Temporal Ctx | 15.3 | Control (Path) 1 Occipital Ctx | 89.5 |
| AD 5 Inf Temporal Ctx | 89.5 | Control (Path) 2 Occipital Ctx | 8.2 |
| AD 5 Sup Temporal Ctx | 35.8 | Control (Path) 3 Occipital Ctx | 0.6 |
| AD 6 Inf Temporal Ctx | 27.4 | Control (Path) 4 Occipital Ctx | 10.3 |
| AD 6 Sup Temporal Ctx | 32.8 | Control 1 Parietal Ctx | 3.6 |
| Control 1 Temporal Ctx | 3.4 | Control 2 Parietal Ctx | 23.7 |
| Control 2 Temporal Ctx | 47.6 | Control 3 Parietal Ctx | 14.1 |
| Control 3 Temporal Ctx | 12.4 | Control (Path) 1 Parietal Ctx | 100.0 |
| Control 3 Temporal Ctx | 5.8 | Control (Path) 2 Parietal Ctx | 21.9 |
| Control (Path) 1 Temporal Ctx | 64.2 | Control (Path) 3 Parietal Ctx | 2.0 |
| Control (Path) 2 | .. | Control (Path) 4 | .. |

Table 3: General Statistics

| Tissue Name | Rel. Exp.(%) Ag3337, Run 215773748 | Tissue Name | Rel. Exp.(%) Ag3337, Run 215773748 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 20.2 | Renal ca. TK-10 | 22.1 |
| Melanoma* Hs688(A).T | 58.6 | Bladder | 14.2 |
| Melanoma* Hs688(B).T | 22.8 | Gastric ca. (liver met.) NCI-N87 | 16.2 |
| Melanoma* M14 | 5.7 | Gastric ca. KATO III | 100.0 |
| Melanoma* LOXIMVI | 5.5 | Colon ca. SW-948 | 16.3 |
| Melanoma* SK- MEL-5 | 3.4 | Colon ca. SW480 | 4.2 |
| Squamous cell carcinoma SCC-4 | 4.4 | Colon ca.* (SW480 met) SW620 | 2.6 |
| Testis Pool | 5.1 | Colon ca. HT29 | 0.7 |
| Prostate ca.* (bone met) PC-3 | 6.4 | Colon ca. HCT-116 | 7.6 |
| Prostate Pool | 3.4 | Colon ca. CaCo-2 | 81.8 |
| Placenta | 1.6 | Colon cancer tissue | 1.7 |
| Uterus Pool | 2.1 | Colon ca. SW1116 | 1.6 |
| Ovarian ca. OVCAR-3 | 8.9 | Colon ca. Colo-205 | 0.1 |
| Ovarian ca. SK-OV- 3 | 32.1 | Colon ca. SW-48 | 3.2 |
| Ovarian ca. OVCAR-4 | 7.2 | Colon Pool | 8.0 |
| Ovarian ca. OVCAR-5 | 21.0 | Small Intestine Pool | 7.9 |
| Ovarian ca. IGROV- 1 | 23.5 | Stomach Pool | 5.7 |
| Ovarian ca. OVCAR-8 | 5.4 | Bone Marrow Pool | 3.8 |
| Ovary | 11.7 | Fetal Heart | 24.8 |
| Breast ca. MCF-7 | 5.1 | Heart Pool | 10.2 |
| Breast ca. MDA- MB-231 | 19.5 | Lymph Node Pool | 10.6 |
| Breast ca. BT 549 | 11.7 | Fetal Skeletal Muscle | 30.1 |
| Breast ca. T47D | 30.8 | Skeletal Muscle Pool | 24.8 |
| Breast ca. MDA-N | 5.0 | Spleen Pool | 2.9 |
| Breast Pool | 6.9 | Thymus Pool | 0.0 |

| | | | |
|-------------------|------|-----------------------------------|------|
| Fetal Lung | 10.8 | CNS cancer (neuro;met) SK-N-AS | 23.5 |
| Lung ca. NCI-N417 | 0.8 | CNS cancer (astro) SF-539 | 21.5 |
| Lung ca. LX-1 | 1.7 | CNS cancer (astro) SNB-75 | 40.3 |
| Lung ca. NCI-H146 | 0.4 | CNS cancer (glio) SNB-19 | 27.7 |
| Lung ca. SHP-77 | 11.9 | CNS cancer (glio) SF-295 | 38.2 |
| Lung ca. A549 | 13.6 | Brain (Amygdala) Pool | 28.7 |
| Lung ca. NCI-H526 | 7.6 | Brain (cerebellum) | 38.7 |
| Lung ca. NCI-H23 | 10.2 | Brain (fetal) | 58.6 |
| Lung ca. NCI-H460 | 5.1 | Brain (Hippocampus) Pool | 25.7 |
| Lung ca. HOP-62 | 3.8 | Cerebral Cortex Pool | 59.0 |
| Lung ca. NCI-H522 | 10.1 | Brain (Substantia nigra) Pool | 39.2 |
| Liver | 0.3 | Brain (Thalamus) Pool | 51.4 |
| Fetal Liver | 15.3 | Brain (whole) | 58.2 |
| Liver ca. HepG2 | 53.2 | Spinal Cord Pool | 18.6 |
| Kidney Pool | 18.4 | Adrenal Gland | 11.1 |
| Fetal Kidney | 11.4 | Pituitary gland Pool | 4.7 |
| Renal ca. 786-0 | 31.0 | Salivary Gland | 14.0 |
| Renal ca. A498 | 0.7 | Thyroid (female) | 4.9 |
| Renal ca. ACHN | 20.3 | Pancreatic ca. CAPAN2 | 7.5 |
| Renal ca. UO-31 | 8.1 | Pancreas Pool | 9.4 |

Table YD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3337, Run 165725932 | Tissue Name | Rel. Exp.(%) Ag3337, Run 165725932 |
|--------------------|---|-----------------------------|---|
| Secondary Th1 act | 0.0 | HUVEC IL-1beta | 0.7 |
| Secondary Th2 act | 0.0 | HUVEC IFN gamma | 3.9 |
| Secondary Tr1 act | 0.4 | HUVEC TNF alpha + IFN gamma | 0.3 |
| Secondary Th1 rest | 0.4 | HUVEC TNF alpha + IL4 | 0.6 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.3 |

Lung Microvascular EC

| Primary Th1 act | IFNalpha + IL-1beta | Microvascular Dermal EC | 16.4 |
|-----------------|---------------------|-------------------------|------|
| Primary Th2 act | 1.3 | | |

| | | | |
|--------------------------------|------|--|-------|
| | | none | |
| Primary Tr1 act | 0.6 | Microvasular Dermal EC TNFalpha + IL-1beta | 9.8 |
| Primary Th1 rest | 1.3 | Bronchial epithelium TNFalpha + IL1beta | 1.2 |
| Primary Th2 rest | 0.6 | Small airway epithelium none | 1.3 |
| Primary Tr1 rest | 0.3 | Small airway epithelium TNFalpha + IL-1beta | 2.1 |
| CD45RA CD4 lymphocyte act | 18.7 | Coronery artery SMC rest | 9.9 |
| CD45RO CD4 lymphocyte act | 0.6 | Coronery artery SMC TNFalpha + IL-1beta | 3.5 |
| CD8 lymphocyte act | 1.2 | Astrocytes rest | 100.0 |
| Secondary CD8 lymphocyte rest | 0.9 | Astrocytes TNFalpha + IL-1beta | 65.5 |
| Secondary CD8 lymphocyte act | 0.2 | KU-812 (Basophil) rest | 11.7 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 8.5 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.3 | CCD1106 (Keratinocytes) none | 2.0 |
| LAK cells rest | 4.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 2.0 |
| LAK cells IL-2 | 1.2 | Liver cirrhosis | 3.6 |
| LAK cells IL-2+IL-12 | 0.4 | Lupus kidney | 13.6 |
| LAK cells IL-2+IFN gamma | 2.1 | NCI-H292 none | 11.0 |
| LAK cells IL-2+ IL-18 | 1.2 | NCI-H292 IL-4 | 25.0 |
| LAK cells PMA/ionomycin | 2.0 | NCI-H292 IL-9 | 15.6 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 12.5 |
| Two Way MLR 3 day | 5.2 | NCI-H292 IFN gamma | 4.6 |
| Two Way MLR 5 day | 2.7 | HPAEC none | 1.5 |
| Two Way MLR 7 day | 1.8 | HPAEC TNF alpha + IL-1 beta | 2.5 |
| PBMC rest | 0.2 | Lung fibroblast none | 80.1 |
| PBMC PWM | 1.9 | Lung fibroblast TNF alpha + IL-1 beta | 22.7 |
| PBMC PHA-L | 0.3 | Lung fibroblast IL-4 | 97.3 |
| Ramos (B cell) none | ? | Lung fibroblast IL-9 | 17.7 |

| | | | |
|-------------------|-----|---------------------------|------|
| B lymphocytes PWM | 0.7 | Lung fibroblast IFN gamma | 50.7 |
|-------------------|-----|---------------------------|------|

| | | | |
|------------------------------|------|-------------------------------------|------|
| B lymphocytes CD40L and IL-4 | 0.6 | Dermal fibroblast CCD1070 rest | 94.6 |
| EOL-1 dbcAMP | 4.9 | Dermal fibroblast CCD1070 TNF alpha | 43.2 |
| EOL-1 dbcAMP PMA/ionomycin | 1.2 | Dermal fibroblast CCD1070 IL-1 beta | 31.2 |
| Dendritic cells none | 12.8 | Dermal fibroblast IFN gamma | 14.2 |
| Dendritic cells LPS | 1.3 | Dermal fibroblast IL-4 | 95.9 |
| Dendritic cells anti-CD40 | 11.4 | IBD Colitis 2 | 1.2 |
| Monocytes rest | 0.5 | IBD Crohn's | 9.1 |
| Monocytes LPS | 1.3 | Colon | 60.7 |
| Macrophages rest | 13.6 | Lung | 8.0 |
| Macrophages LPS | 2.8 | Thymus | 39.2 |
| HUVEC none | 1.0 | Kidney | 10.4 |
| HUVEC starved | 1.6 | | . |

CNS_neurodegeneration_v1.0 Summary: Ag3337 - This panel confirms the expression of this gene at low to moderate levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders

General_screening_panel_v1.4 Summary: Ag3337 - This gene is expressed in almost all samples on this panel. This gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

In addition, this gene is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Panel 4D Summary: Ag3337 This gene is most highly expressed in resting astrocytes

expression or function of this gene may be effective in the treatment of pathological and inflammatory lung and skin diseases, such as psoriasis, asthma, emphysema, and allergies.

Z. CG57551-01: NAC-1 Like Gene

Expression of gene CG57551-01 was assessed using the primer-probe set Ag3282, described in Table ZA. Results of the RTQ-PCR runs are shown in Tables ZB, ZC and ZD.

Table ZA. Probe Name Ag3282

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-cagatcctcagcttctgtaca-3' | 22 | 269 | 469 |
| Probe | TET-5'-accagttcctgctcatgtacacggct-3' - TAMRA | 26 | 318 | 470 |
| Reverse | 5'-atctcctggatctgcaggaa-3' | 20 | 347 | 471 |

Table ZB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3282, Run 210060482 | Tissue Name | Rel. Exp.(%) Ag3282, Run 210060482 |
|---------------------------|---------------------------------------|-----------------------------------|---------------------------------------|
| AD 1 Hippo | 22.8 | Control (Path) 3 Temporal Ctx | 9.7 |
| AD 2 Hippo | 49.0 | Control (Path) 4 Temporal Ctx | 24.3 |
| AD 3 Hippo | 11.5 | AD 1 Occipital Ctx | 16.5 |
| AD 4 Hippo | 12.3 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 hippo | 66.9 | AD 3 Occipital Ctx | 10.2 |
| AD 6 Hippo | 59.9 | AD 4 Occipital Ctx | 18.2 |
| Control 2 Hippo | 49.3 | AD 5 Occipital Ctx | 9.5 |
| Control 4 Hippo | 18.7 | AD 6 Occipital Ctx | 41.5 |
| Control (Path) 3 Hippo | 6.3 | Control 1 Occipital Ctx | 6.8 |
| AD 1 Temporal Ctx | 19.2 | Control 2 Occipital Ctx | 91.4 |
| AD 2 Temporal Ctx | 40.3 | Control 3 Occipital Ctx | 16.3 |
| AD 3 Temporal Ctx | 14.3 | Control 4 Occipital Ctx | 12.2 |
| AD 5 Int Temporal Ctx | 66.0 | Control (Path) 2 Occipital Ctx | 9.2 |

| | | | |
|-------------------------------|------|--------------------------------|------|
| AD 5 SupTemporal Ctx | 37.4 | Control (Path) 3 Occipital Ctx | 5.3 |
| AD 6 Inf Temporal Ctx | 36.1 | Control (Path) 4 Occipital Ctx | 15.8 |
| AD 6 Sup Temporal Ctx | 34.4 | Control 1 Parietal Ctx | 11.7 |
| Control 1 Temporal Ctx | 10.0 | Control 2 Parietal Ctx | 34.2 |
| Control 2 Temporal Ctx | 74.7 | Control 3 Parietal Ctx | 23.3 |
| Control 3 Temporal Ctx | 15.0 | Control (Path) 1 Parietal Ctx | 72.7 |
| Control 4 Temporal Ctx | 15.5 | Control (Path) 2 Parietal Ctx | 21.6 |
| Control (Path) 1 Temporal Ctx | 74.2 | Control (Path) 3 Parietal Ctx | 5.5 |
| Control (Path) 2 Temporal Ctx | 31.2 | Control (Path) 4 Parietal Ctx | 35.8 |

Table ZC. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3282, Run 216512995 | Tissue Name | Rel. Exp.(%) Ag3282, Run 216512995 |
|-------------------------------|------------------------------------|----------------------------------|------------------------------------|
| Adipose | 1.8 | Renal ca. TK-10 | 22.7 |
| Melanoma* Hs688(A).T | 16.3 | Bladder | 6.3 |
| Melanoma* Hs688(B).T | 25.0 | Gastric ca. (liver met.) NCI-N87 | 47.0 |
| Melanoma* M14 | 25.3 | Gastric ca. KATO III | 45.7 |
| Melanoma* LOXIMVI | 21.6 | Colon ca. SW-948 | 19.3 |
| Melanoma* SK-MEL-5 | 17.0 | Colon ca. SW480 | 50.3 |
| Squamous cell carcinoma SCC-4 | 24.7 | Colon ca.* (SW480 met) SW620 | 25.9 |
| Testis Pool | 6.1 | Colon ca. HT29 | 17.7 |
| Prostate ca.* (bone met) PC-3 | 67.8 | Colon ca. HCT-116 | 100.0 |
| Prostate Pool | 3.5 | Colon ca. CaCo-2 | 29.1 |
| Placenta | 9.6 | Colon cancer tissue | 14.0 |

| | | | |
|---------------------|------|----------------|-----|
| Ovarian ca. SK-OV-3 | 65.5 | Colon ca. SW48 | 5.8 |
|---------------------|------|----------------|-----|

| | | | |
|------------------------|------|-------------------------------------|-------|
| Ovarian ca. OVCAR-4 | 35.8 | Colon Pool | 4.9 |
| Ovarian ca. OVCAR-5 | 37.6 | Small Intestine Pool | 2.4 |
| Ovarian ca. IGROV-1 | 28.9 | Stomach Pool | 3.3 |
| Ovarian ca. OVCAR-8 | 14.2 | Bone Marrow Pool | 1.5 |
| Ovary | 3.9 | Fetal Heart | 3.0 |
| Breast ca. MCF-7 | 42.3 | Heart Pool | 2.2 |
| Breast ca. MDA-MB-231 | 69.7 | Lymph Node Pool | 5.6 |
| Breast ca. BT 549 | 51.4 | Fetal Skeletal Muscle | 1.5 |
| Breast ca. T47D | 86.5 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 26.4 | Spleen Pool | 2.8 |
| Breast Pool | 4.6 | Thymus Pool | 3.8 |
| Trachea | 8.7 | CNS cancer (glio/astro) U87-MG | 60.3 |
| Lung | 0.2 | CNS cancer (glio/astro) U-118-MG | 100.0 |
| Fetal Lung | 6.3 | CNS cancer (neuro;met) SK-N-AS | 47.3 |
| Lung ca. NCI-N417 | 8.4 | CNS cancer (astro) SF-539 | 22.8 |
| Lung ca. LX-1 | 17.3 | CNS cancer (astro) SNB-75 | 47.3 |
| Lung ca. NCI-H146 | 15.3 | CNS cancer (glio) SNB-19 | 29.3 |
| Lung ca. SHP-77 | 16.5 | CNS cancer (glio) SF-295 | 49.3 |
| Lung ca. A549 | 27.2 | Brain (Amygdala) Pool | 6.9 |
| Lung ca. NCI-H526 | 6.1 | Brain (cerebellum) | 15.1 |
| Lung ca. NCI-H23 | 25.9 | Brain (fetal) | 9.2 |
| Lung ca. NCI-H460 | 8.0 | Brain (Hippocampus) Pool | 8.9 |
| Lung ca. HOP-62 | 11.9 | Cerebral Cortex Pool | 13.4 |
| Lung ca. NCI-H522 | 21.9 | Brain (Substantia nigra) Pool | 15.3 |
| Liver | 1.7 | Brain (Thalamus) Pool | 11.5 |
| Fetal Liver | 9.8 | Brain (whole) | 12.6 |

| | | | |
|-----------------|------|----------------------|-----|
| Fetal Kidney | 4 | Pituitary gland Pool | 1 |
| Renal ca. 786-0 | 42.0 | Salivary Gland | 4.0 |

| | | | |
|-----------------|------|-----------------------|------|
| Renal ca. A498 | 16.7 | Thyroid (female) | 3.6 |
| Renal ca. ACHN | 13.9 | Pancreatic ca. CAPAN2 | 15.5 |
| Renal ca. UO-31 | 17.4 | Pancreas Pool | 6.6 |

Table ZD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3282, Run 164634321 | Tissue Name | Rel. Exp.(%) Ag3282, Run 164634321 |
|-------------------------------|--|---|--|
| Secondary Th1 act | 52.9 | HUVEC IL-1beta | 13.6 |
| Secondary Th2 act | 67.8 | HUVEC IFN gamma | 42.9 |
| Secondary Tr1 act | 75.3 | HUVEC TNF alpha + IFN gamma | 37.1 |
| Secondary Th1 rest | 8.4 | HUVEC TNF alpha + IL4 | 42.6 |
| Secondary Th2 rest | 11.4 | HUVEC IL-11 | 25.9 |
| Secondary Tr1 rest | 12.2 | Lung Microvascular EC none | 41.2 |
| Primary Th1 act | 53.6 | Lung Microvascular EC TNFalpha + IL-1beta | 36.3 |
| Primary Th2 act | 44.4 | Microvascular Dermal EC none | 50.3 |
| Primary Tr1 act | 60.7 | Microvasular Dermal EC TNFalpha + IL-1beta | 33.0 |
| Primary Th1 rest | 37.6 | Bronchial epithelium TNFalpha + IL1beta | 51.4 |
| Primary Th2 rest | 15.8 | Small airway epithelium none | 23.3 |
| Primary Tr1 rest | 18.3 | Small airway epithelium TNFalpha + IL-1beta | 71.7 |
| CD45RA CD4 lymphocyte act | 33.0 | Coronery artery SMC rest | 43.5 |
| CD45RO CD4 lymphocyte act | 54.7 | Coronery artery SMC TNFalpha + IL-1beta | 31.0 |
| CD8 lymphocyte act | 42.9 | Astrocytes rest | 38.4 |
| Secondary CD8 lymphocyte rest | 50.3 | Astrocytes TNFalpha + IL-1beta | 37.1 |
| Secondary CD8 lymphocyte act | 32.5 | KU-812 (Basophil) rest | 36.1 |
| CD4 lymphocyte none | 2.4 | KU-812 (Basophil) PMA/ionomycin | 90.8 |

Primary Th1 Th2 Th1 rest Th2 rest Tr1 act Tr1 rest Tr2 act Tr2 rest CD45RA CD4 lymphocyte act CD45RO CD4 lymphocyte act CD8 lymphocyte act Secondary CD8 lymphocyte rest Secondary CD8 lymphocyte act CD4 lymphocyte none

| Antigen | Rel. Exp.(%) Ag3282, Run 164634321 | Antigen | Rel. Exp.(%) Ag3282, Run 164634321 |
|----------------|--|---------------------|--|
| LAK cells IL-2 | 41.2 | IFNalpha + IL-1beta | 2.9 |

| | | | |
|------------------------------|-------|---------------------------------------|------|
| LAK cells IL-2+IL-12 | 29.5 | Lupus kidney | 2.2 |
| LAK cells IL-2+IFN gamma | 36.3 | NCI-H292 none | 38.4 |
| LAK cells IL-2+ IL-18 | 34.2 | NCI-H292 IL-4 | 66.9 |
| LAK cells PMA/ionomycin | 11.8 | NCI-H292 IL-9 | 62.4 |
| NK Cells IL-2 rest | 29.3 | NCI-H292 IL-13 | 65.1 |
| Two Way MLR 3 day | 21.9 | NCI-H292 IFN gamma | 48.3 |
| Two Way MLR 5 day | 27.7 | HPAEC none | 31.2 |
| Two Way MLR 7 day | 27.0 | HPAEC TNF alpha + IL-1 beta | 37.6 |
| PBMC rest | 6.5 | Lung fibroblast none | 35.6 |
| PBMC PWM | 89.5 | Lung fibroblast TNF alpha + IL-1 beta | 20.7 |
| PBMC PHA-L | 53.6 | Lung fibroblast IL-4 | 63.3 |
| Ramos (B cell) none | 40.6 | Lung fibroblast IL-9 | 55.5 |
| Ramos (B cell) ionomycin | 56.3 | Lung fibroblast IL-13 | 44.8 |
| B lymphocytes PWM | 100.0 | Lung fibroblast IFN gamma | 71.2 |
| B lymphocytes CD40L and IL-4 | 41.2 | Dermal fibroblast CCD1070 rest | 78.5 |
| EOL-1 dbcAMP | 50.0 | Dermal fibroblast CCD1070 TNF alpha | 88.9 |
| EOL-1 dbcAMP PMA/ionomycin | 46.3 | Dermal fibroblast CCD1070 IL-1 beta | 49.7 |
| Dendritic cells none | 33.2 | Dermal fibroblast IFN gamma | 21.5 |
| Dendritic cells LPS | 26.1 | Dermal fibroblast IL-4 | 43.8 |
| Dendritic cells anti-CD40 | 29.9 | IBD Colitis 2 | 1.2 |
| Monocytes rest | 17.1 | IBD Crohn's | 1.8 |
| Monocytes LPS | 14.0 | Colon | 15.4 |
| Macrophages rest | 59.0 | Lung | 16.6 |
| Macrophages LPS | 29.1 | Thymus | 15.6 |
| HUVEC none | 35.1 | Kidney | 18.9 |
| HUVEC starved | 62.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3282 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no

trans and those of non-temperate countries this experiment. Please see Panel 4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3282 Highest expression of this gene is seen in a brain cancer cell line (CT=24.3). This gene appears to be expressed more highly in the cancer cell lines than in the normal tissue samples on this panel and may be involved in cellular growth and proliferation. Based on this expression profile, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene is also expressed at high levels in all regions of the CNS examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

In addition, this gene product is expressed in adipose, pancreas, adrenal, thyroid, pituitary, fetal skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Furthermore, this gene is more highly expressed in fetal skeletal muscle (CT=30.4) and liver (CT=27) when compared to expression in the adult skeletal muscle (CT>35) and liver (CT=30) may be useful for the differentiation of the fetal and adult sources of this tissue.

Panel 4D Summary: Ag3282 This gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. Highest expression is seen in polkweed mitogen stimulated B lymphocytes (CT=25.7). In addition, expression is seen in members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in Panel 1.4 and also suggests a role for the gene product in cell

improvement of the symptoms of patients suffering from autoimmune and inflammatory

diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AA. CG57411-01: KELCH-LIKE PROTEIN KLHL3C

Expression of gene CG57411-01 was assessed using the primer-probe set Ag3229, described in Table AAA. Results of the RTQ-PCR runs are shown in Tables AAB, AAC, AAD and AAE.

Table AAA. Probe Name Ag3229

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-gcagcgagcttaccacat-3' | 19 | 287 | 472 |
| Probe | TET-5'-aaggcccttcgcgctgcagatctt-3' - TAMRA | 23 | 310 | 473 |
| Reverse | 5'-aagtgcgtcctggagatgct-3' | 20 | 364 | 474 |

Table AAB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3229, Run 209862301 | Tissue Name | Rel. Exp.(%) Ag3229, Run 209862301 |
|---------------------------|---------------------------------------|----------------------------------|---------------------------------------|
| AD 1 Hippo | 16.3 | Control (Path) 3 Temporal Ctx | 8.0 |
| AD 2 Hippo | 34.6 | Control (Path) 4 Temporal Ctx | 35.8 |
| AD 3 Hippo | 15.9 | AD 1 Occipital Ctx | 18.6 |
| AD 4 Hippo | 6.9 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 Hippo | 100.0 | AD 3 Occipital Ctx | 11.7 |
| AD 6 Hippo | 35.4 | AD 4 Occipital Ctx | 17.7 |
| Control 2 Hippo | 31.2 | AD 5 Occipital Ctx | 49.7 |
| Control 4 Hippo | 12.1 | AD 6 Occipital Ctx | 14.2 |
| Control (Path) 3 Hippo | 6.2 | Control 1 Occipital Ctx | 3.3 |
| AD 1 Temporal Ctx | 21.6 | Control 2 Occipital Ctx | 69.3 |

| | | | |
|-------------------|------|----------------------------|-----|
| AD 3 Temporal Ctx | 14.1 | Control 4 Occipital Ctx | 1.7 |
|-------------------|------|----------------------------|-----|

| | | | |
|----------------------------------|------|-----------------------------------|------|
| AD 4 Temporal Ctx | 16.8 | Control (Path) 1 Occipital Ctx | 72.2 |
| AD 5 Inf Temporal Ctx | 71.7 | Control (Path) 2 Occipital Ctx | 13.7 |
| AD 5 Sup Temporal Ctx | 32.3 | Control (Path) 3 Occipital Ctx | 6.3 |
| AD 6 Inf Temporal Ctx | 30.6 | Control (Path) 4 Occipital Ctx | 16.8 |
| AD 6 Sup Temporal Ctx | 33.9 | Control 1 Parietal Ctx | 8.6 |
| Control 1 Temporal Ctx | 4.4 | Control 2 Parietal Ctx | 39.8 |
| Control 2 Temporal Ctx | 56.6 | Control 3 Parietal Ctx | 21.5 |
| Control 3 Temporal Ctx | 19.6 | Control (Path) 1 Parietal Ctx | 66.4 |
| Control 3 Temporal Ctx | 14.2 | Control (Path) 2 Parietal Ctx | 26.8 |
| Control (Path) 1 Temporal Ctx | 62.0 | Control (Path) 3 Parietal Ctx | 5.2 |
| Control (Path) 2 Temporal Ctx | 36.1 | Control (Path) 4 Parietal Ctx | 54.3 |

Table AAC. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3229, Run 214439727 | Tissue Name | Rel. Exp.(%) Ag3229, Run 214439727 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 6.0 | Renal ca. TK-10 | 20.4 |
| Melanoma* Hs688(A).T | 8.1 | Bladder | 6.7 |
| Melanoma* Hs688(B).T | 13.5 | Gastric ca. (liver met.) NCI-N87 | 11.2 |
| Melanoma* M14 | 2.1 | Gastric ca. KATO III | 59.5 |
| Melanoma* LOXIMVI | 24.8 | Colon ca. SW-948 | 0.6 |
| Melanoma* SK-MEL-5 | 20.7 | Colon ca. SW480 | 31.6 |
| Squamous cell carcinoma SCC-4 | 6.7 | Colon ca.* (SW480 met) SW620 | 4.7 |
| Testis Pool | 3.0 | Colon ca. HT29 | 2.7 |
| Prostate ca * (bone) | | | |

| | | | |
|-------------|-----|---------------------|-----|
| Placenta | + | colon cancer tissue | + |
| Uterus Pool | 5.8 | Colon ca. SW1116 | 3.3 |

| | | | |
|------------------------|--------------|-------------------------------------|------|
| Ovarian ca. OVCAR-3 | 40.9 | Colon ca. Colo-205 | 5.4 |
| Ovarian ca. SK-OV-3 | 17.7 | Colon ca. SW-48 | 3.3 |
| Ovarian ca. OVCAR-4 | 11.9 | Colon Pool | 25.0 |
| Ovarian ca. OVCAR-5 | 84.1 | Small Intestine Pool | 14.9 |
| Ovarian ca. IGROV-1 | 2.0 | Stomach Pool | 6.4 |
| Ovarian ca. OVCAR-8 | 8.1 | Bone Marrow Pool | 9.7 |
| Ovary | 8.7 | Fetal Heart | 1.7 |
| Breast ca. MCF-7 | 0.9 | Heart Pool | 10.7 |
| Breast ca. MDA-MB-231 | 30.1 | Lymph Node Pool | 21.8 |
| Breast ca. BT 549 | 8.1 | Fetal Skeletal Muscle | 4.2 |
| Breast ca. T47D | 100.0 | Skeletal Muscle Pool | 8.7 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 10.4 |
| Breast Pool | 22.4 | Thymus Pool | 11.2 |
| Trachea | 10.4 | CNS cancer (glio/astro) U87-MG | 55.5 |
| Lung | 1.7 | CNS cancer (glio/astro) U-118-MG | 44.8 |
| Fetal Lung | 6.7 | CNS cancer (neuro;met) SK-N-AS | 5.8 |
| Lung ca. NCI-N417 | 11.7 | CNS cancer (astro) SF-539 | 0.4 |
| Lung ca. LX-1 | 37.1 | CNS cancer (astro) SNB-75 | 5.0 |
| Lung ca. NCI-H146 | 6.2 | CNS cancer (glio) SNB-19 | 2.9 |
| Lung ca. SHP-77 | 61.1 | CNS cancer (glio) SF-295 | 39.0 |
| Lung ca. A549 | 6.3 | Brain (Amygdala) Pool | 8.4 |
| Lung ca. NCI-H526 | 8.7 | Brain (cerebellum) | 22.2 |
| Lung ca. NCI-H23 | 6.3 | Brain (fetal) | 48.6 |
| Lung ca. NCI-H460 | 2.9 | Brain (Hippocampus) Pool | 8.5 |
| Lung ca. HOP-62 | 8.1 | Cerebral Cortex Pool | 20.7 |

Drugs & Chemicals

| | DRUGS & CHEMICALS | |
|-------------|-------------------|---------------|
| Fetal Liver | 1.8 | Brain (whole) |

| | | | |
|-----------------|------|-----------------------|------|
| Liver ca. HepG2 | 0.2 | Spinal Cord Pool | 3.3 |
| Kidney Pool | 26.8 | Adrenal Gland | 29.9 |
| Fetal Kidney | 10.2 | Pituitary gland Pool | 10.7 |
| Renal ca. 786-0 | 7.5 | Salivary Gland | 4.1 |
| Renal ca. A498 | 4.0 | Thyroid (female) | 1.1 |
| Renal ca. ACHN | 11.9 | Pancreatic ca. CAPAN2 | 1.0 |
| Renal ca. UO-31 | 15.3 | Pancreas Pool | 28.7 |

Table AAD. Panel 2.2

| Tissue Name | Rel. Exp.(%) Ag3229, Run 174442765 | Tissue Name | Rel. Exp.(%) Ag3229, Run 174442765 |
|--------------------------------------|--|---|--|
| Normal Colon | 15.5 | Kidney Margin (OD04348) | 100.0 |
| Colon cancer (OD06064) | 31.9 | Kidney malignant cancer (OD06204B) | 10.7 |
| Colon Margin (OD06064) | 20.6 | Kidney normal adjacent tissue (OD06204E) | 11.6 |
| Colon cancer (OD06159) | 6.0 | Kidney Cancer (OD04450-01) | 38.4 |
| Colon Margin (OD06159) | 12.7 | Kidney Margin (OD04450-03) | 17.4 |
| Colon cancer (OD06297-04) | 3.7 | Kidney Cancer 8120613 | 0.0 |
| Colon Margin (OD06297-05) | 22.4 | Kidney Margin 8120614 | 6.0 |
| CC Gr.2 ascend colon (ODO3921) | 6.5 | Kidney Cancer 9010320 | 12.0 |
| CC Margin (ODO3921) | 10.5 | Kidney Margin 9010321 | 9.9 |
| Colon cancer metastasis (OD06104) | 8.6 | Kidney Cancer 8120607 | 47.3 |
| Lung Margin (OD06104) | 6.2 | Kidney Margin 8120608 | 5.6 |
| Colon mets to lung (OD04451-01) | 31.0 | Normal Uterus | 48.3 |
| Lung Margin (OD04451-02) | 39.5 | Uterine Cancer 064011 | 14.9 |
| Normal Prostate | 41.2 | Normal Thyroid | 2.6 |

| | | | |
|------------------------------|---------|----------------|-----|
| Prostate Margin (OD04410) | A302152 | Thyroid Margin | 2.7 |
| Normal Ovary | 23.2 | | |

| | | | |
|--|------|--|------|
| | | A302153 | |
| Ovarian cancer (OD06283-03) | 7.2 | Normal Breast | 46.0 |
| Ovarian Margin (OD06283-07) | 17.8 | Breast Cancer (OD04566) | 5.9 |
| Ovarian Cancer 064008 | 22.2 | Breast Cancer 1024 | 27.4 |
| Ovarian cancer (OD06145) | 9.0 | Breast Cancer (OD04590-01) | 19.5 |
| Ovarian Margin (OD06145) | 13.4 | Breast Cancer Mets (OD04590-03) | 13.5 |
| Ovarian cancer (OD06455-03) | 6.3 | Breast Cancer Metastasis (OD04655-05) | 12.2 |
| Ovarian Margin (OD06455-07) | 12.9 | Breast Cancer 064006 | 8.1 |
| Normal Lung | 14.5 | Breast Cancer 9100266 | 3.0 |
| Invasive poor diff. lung adeno (ODO4945-01) | 5.0 | Breast Margin 9100265 | 3.4 |
| Lung Margin (ODO4945-03) | 37.4 | Breast Cancer A209073 | 11.2 |
| Lung Malignant Cancer (OD03126) | 9.6 | Breast Margin A2090734 | 61.1 |
| Lung Margin (OD03126) | 14.2 | Breast cancer (OD06083) | 4.7 |
| Lung Cancer (OD05014A) | 4.9 | Breast cancer node metastasis (OD06083) | 12.7 |
| Lung Margin (OD05014B) | 39.0 | Normal Liver | 2.8 |
| Lung cancer (OD06081) | 17.4 | Liver Cancer 1026 | 13.6 |
| Lung Margin (OD06081) | 32.3 | Liver Cancer 1025 | 12.9 |
| Lung Cancer (OD04237-01) | 4.2 | Liver Cancer 6004-T | 13.2 |
| Lung Margin (OD04237-02) | 24.7 | Liver Tissue 6004-N | 1.3 |
| Ocular Melanoma Metastasis | 12.9 | Liver Cancer 6005-T | 43.2 |
| Ocular Melanoma Margin (Liver) | 10.7 | Liver Tissue 6005-N | 4.8 |
| Melanoma Metastasis | 52.9 | Liver Cancer 064003 | 39.5 |
| Melanoma Margin | | | |

| | | | |
|---|------|---------------------------|-----|
| Kidney Ca. Nucleus grade 2 (OD04338) | 40.3 | Bladder Cancer A302173 | 4.2 |
|---|------|---------------------------|-----|

| | | | |
|--|------|---------------------------|------|
| Kidney Margin (OD04338) | 7.5 | Normal Stomach | 31.4 |
| Kidney Ca Nuclear grade 1/2 (OD04339) | 82.4 | Gastric Cancer 9060397 | 1.2 |
| Kidney Margin (OD04339) | 13.2 | Stomach Margin 9060396 | 7.1 |
| Kidney Ca, Clear cell type (OD04340) | 8.3 | Gastric Cancer 9060395 | 7.4 |
| Kidney Margin (OD04340) | 24.7 | Stomach Margin 9060394 | 10.9 |
| Kidney Ca, Nuclear grade 3 (OD04348) | 13.1 | Gastric Cancer 064005 | 10.4 |

Table AAE. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3229, Run 164389704 | Tissue Name | Rel. Exp.(%) Ag3229, Run 164389704 |
|----------------------------------|--|--|--|
| Secondary Th1 act | 3.4 | HUVEC IL-1beta | 20.0 |
| Secondary Th2 act | 4.8 | HUVEC IFN gamma | 32.5 |
| Secondary Tr1 act | 2.1 | HUVEC TNF alpha + IFN gamma | 26.6 |
| Secondary Th1 rest | 1.2 | HUVEC TNF alpha + IL4 | 35.1 |
| Secondary Th2 rest | 2.0 | HUVEC IL-11 | 17.6 |
| Secondary Tr1 rest | 4.5 | Lung Microvascular EC none | 34.2 |
| Primary Th1 act | 17.7 | Lung Microvascular EC TNFalpha + IL-1beta | 49.0 |
| Primary Th2 act | 5.3 | Microvascular Dermal EC none | 30.6 |
| Primary Tr1 act | 25.9 | Microvascular Dermal EC TNFalpha + IL-1beta | 38.7 |
| Primary Th1 rest | 14.0 | Bronchial epithelium TNFalpha + IL1beta | 46.7 |
| Primary Th2 rest | 6.5 | Small airway epithelium none | 22.1 |
| Primary Tr1 rest | 22.1 | Small airway epithelium TNFalpha + IL-1beta | 97.9 |
| CD45RA CD4 lymphocyte act | 12.7 | Coronery artery SMC rest | 31.2 |
| CD45RO CD4 | | Coronery artery SMC | |
| Secondary CD8 lymphocyte rest | 4.2 | Astrocytes TNFalpha IL-1beta | 5.0 |

| | | | |
|--------------------------------|------|--|-------|
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.8 |
| CD4 lymphocyte none | 5.6 | KU-812 (Basophil) PMA/ionomycin | 2.9 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 3.7 | CCD1106 (Keratinocytes) none | 6.2 |
| LAK cells rest | 5.9 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 6.0 |
| LAK cells IL-2 | 3.0 | Liver cirrhosis | 15.5 |
| LAK cells IL-2+IL-12 | 6.2 | Lupus kidney | 12.2 |
| LAK cells IL-2+IFN gamma | 10.7 | NCI-H292 none | 30.8 |
| LAK cells IL-2+ IL-18 | 5.0 | NCI-H292 IL-4 | 49.7 |
| LAK cells PMA/ionomycin | 4.0 | NCI-H292 IL-9 | 43.5 |
| NK Cells IL-2 rest | 1.9 | NCI-H292 IL-13 | 31.6 |
| Two Way MLR 3 day | 9.0 | NCI-H292 IFN gamma | 17.7 |
| Two Way MLR 5 day | 3.3 | HPAEC none | 18.0 |
| Two Way MLR 7 day | 1.2 | HPAEC TNF alpha + IL-1 beta | 58.2 |
| PBMC rest | 0.8 | Lung fibroblast none | 40.6 |
| PBMC PWM | 10.7 | Lung fibroblast TNF alpha + IL-1 beta | 11.0 |
| PBMC PHA-L | 10.2 | Lung fibroblast IL-4 | 100.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 55.1 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 78.5 |
| B lymphocytes PWM | 23.3 | Lung fibroblast IFN gamma | 82.4 |
| B lymphocytes CD40L and IL-4 | 18.6 | Dermal fibroblast CCD1070 rest | 45.4 |
| EOL-1 dbcAMP | 1.8 | Dermal fibroblast CCD1070 TNF alpha | 36.3 |
| EOL-1 dbcAMP PMA/ionomycin | 2.0 | Dermal fibroblast CCD1070 IL-1 beta | 23.8 |
| Dendritic cells none | 5.9 | Dermal fibroblast IFN gamma | 4.6 |
| Dendritic cells LPS | 8.0 | Dermal fibroblast IL-4 | 16.6 |
| Dendritic cells anti-CD40 | 3.3 | IBD Colitis 2 | 6.2 |

| Macrophages rest | LUNG | Thymus | 20.6 |
|------------------|------|--------|------|
| Macrophages LPS | 1.4 | | |

| | | | |
|---------------|------|--------|------|
| HUVEC none | 35.1 | Kidney | 20.9 |
| HUVEC starved | 58.2 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3229 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3229 - Highest levels of expression of this gene are seen in breast cancer cell line T47D (CT=28.5). Based on expression in this panel, this gene may be involved in gastric, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, and heart. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at low to moderate levels in all regions of the CNS examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 2.2 Summary: Ag3229 Highest expression of the CG57411-01 gene is seen in the kidney (CT=32.2). In addition, significant levels of expression are seen in samples derived from normal lung and breast. Expression in these normal tissues is also higher than in the corresponding malignant tissue. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of lung, breast and kidney cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of lung, breast and kidney cancer.

treated lung fibroblasts (CT=31.3). Significant levels of expression are seen in activated-NC1-

H292 mucoepidermoid cells as well as untreated NCI-H292 cells. Moderate expression is also detected in IL-9, IL-13 and IFN gamma activated lung fibroblasts, human pulmonary aortic endothelial cells (treated and untreated), small airway epithelium (treated and untreated), treated bronchial epithelium and lung microvascular endothelial cells (treated and untreated). The expression of this gene in cells derived from or within the lung suggests that this gene may be involved in normal conditions as well as pathological and inflammatory lung disorders that include chronic obstructive pulmonary disease, asthma, allergy and emphysema. Moderate/low expression of this gene is also detected in treated and untreated HUVECs (endothelial cells) and coronary artery smooth muscle cells (treated and untreated) and normal tissues that include lung, colon, thymus and kidney. Expression in the various immune cell types and tissue samples suggests that therapeutic modulation of this gene product may ameliorate symptoms associated with infectious conditions as well as inflammatory and autoimmune disorders that include psoriasis, allergy, asthma, inflammatory bowel disease, rheumatoid arthritis and osteoarthritis.

AB. CG57399-01 and CG57399-03: PHOSPHOLIPASE ADRAB-B PRECURSOR

Expression of gene CG57399-01 and variant CG57399-03 was assessed using the primer-probe sets Ag3952 and Ag3226, described in Tables ABA and ABB. Results of the RTQ-PCR runs are shown in Tables ABC and ABD.

Table ABA. Probe Name Ag3952

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-ctgtgtccctgtgtcctgaa-3' | 20 | 1633 | 475 |
| Probe | TET-5'-tcaacagaacttgctaccctcatcga-3'-TAMRA | 26 | 1666 | 476 |
| Reverse | 5'-gtgggttttcctgaaaacttc-3' | 22 | 1701 | 477 |

Table ABB. Probe Name Ag3226

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-gatgatcctcaggtcactgtgt-3' | 22 | 1617 | 478 |
| Probe | TET-5'-ccctgtgtcctgaagttgtatgataactca-3'-TAMRA | 30 | 1639 | 479 |

| Tissue Name | Rel. Exp.(%) Ag3952, Run 213856126 | Tissue Name | Rel. Exp.(%) Ag3952, Run 213856126 |
|-------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 9.0 | Renal ca. TK-10 | 15.0 |
| Melanoma* Hs688(A).T | 3.0 | Bladder | 22.7 |
| Melanoma* Hs688(B).T | 3.4 | Gastric ca. (liver met.) NCI-N87 | 13.0 |
| Melanoma* M14 | 0.9 | Gastric ca. KATO III | 75.3 |
| Melanoma* LOXIMVI | 11.7 | Colon ca. SW-948 | 4.3 |
| Melanoma* SK-MEL-5 | 1.5 | Colon ca. SW480 | 97.3 |
| Squamous cell carcinoma SCC-4 | 8.7 | Colon ca.* (SW480 met) SW620 | 4.4 |
| Testis Pool | 12.8 | Colon ca. HT29 | 0.4 |
| Prostate ca.* (bone met) PC-3 | 10.5 | Colon ca. HCT-116 | 1.2 |
| Prostate Pool | 12.9 | Colon ca. CaCo-2 | 60.7 |
| Placenta | 5.1 | Colon cancer tissue | 28.7 |
| Uterus Pool | 6.5 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 7.3 | Colon ca. Colo-205 | 0.9 |
| Ovarian ca. SK-OV-3 | 26.4 | Colon ca. SW-48 | 26.1 |
| Ovarian ca. OVCAR-4 | 1.9 | Colon Pool | 18.8 |
| Ovarian ca. OVCAR-5 | 6.7 | Small Intestine Pool | 5.3 |
| Ovarian ca. IGROV-1 | 9.2 | Stomach Pool | 7.9 |
| Ovarian ca. OVCAR-8 | 4.2 | Bone Marrow Pool | 8.4 |
| Ovary | 10.0 | Fetal Heart | 1.2 |
| Breast ca. MCF-7 | 0.4 | Heart Pool | 5.7 |
| Breast ca. MDA-MB-231 | 92.0 | Lymph Node Pool | 32.1 |
| Breast ca. BT 549 | 5.5 | Fetal Skeletal Muscle | 1.2 |
| Breast ca. T47D | 2.5 | Skeletal Muscle Pool | 4.7 |
| Breast ca. MDA-N | 1.6 | Spleen Pool | 18.2 |
| Breast Pool | 19.6 | Thymus Pool | 19.3 |

| | | | |
|-------------------|------|-----------------------------------|-------|
| Fetal Lung | 8.3 | CNS cancer (neuro;met) SK-N-AS | 0.9 |
| Lung ca. NCI-N417 | 0.9 | CNS cancer (astro) SF-539 | 7.6 |
| Lung ca. LX-1 | 27.2 | CNS cancer (astro) SNB-75 | 17.1 |
| Lung ca. NCI-H146 | 10.7 | CNS cancer (glio) SNB-19 | 6.8 |
| Lung ca. SHP-77 | 47.3 | CNS cancer (glio) SF-295 | 5.7 |
| Lung ca. A549 | 5.1 | Brain (Amygdala) Pool | 7.0 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 3.2 |
| Lung ca. NCI-H23 | 4.1 | Brain (fetal) | 19.3 |
| Lung ca. NCI-H460 | 0.5 | Brain (Hippocampus) Pool | 13.1 |
| Lung ca. HOP-62 | 2.7 | Cerebral Cortex Pool | 14.8 |
| Lung ca. NCI-H522 | 1.3 | Brain (Substantia nigra) Pool | 6.3 |
| Liver | 0.0 | Brain (Thalamus) Pool | 15.2 |
| Fetal Liver | 1.7 | Brain (whole) | 10.4 |
| Liver ca. HepG2 | 0.5 | Spinal Cord Pool | 5.3 |
| Kidney Pool | 21.2 | Adrenal Gland | 100.0 |
| Fetal Kidney | 1.6 | Pituitary gland Pool | 4.3 |
| Renal ca. 786-0 | 1.7 | Salivary Gland | 3.4 |
| Renal ca. A498 | 1.3 | Thyroid (female) | 14.5 |
| Renal ca. ACHN | 4.3 | Pancreatic ca. CAPAN2 | 1.7 |
| Renal ca. UO-31 | 17.4 | Pancreas Pool | 24.5 |

Table ABD. Panel 1.3D

| Tissue Name | Rel. Exp.(%) Ag3226, Run 167994701 | Tissue Name | Rel. Exp.(%) Ag3226, Run 167994701 |
|---------------------------|---------------------------------------|-------------------|---------------------------------------|
| Liver adenocarcinoma | 2.5 | Kidney (fetal) | 16.3 |
| Pancreas | 0.0 | Renal ca. 786-0 | 0.9 |
| Pancreatic ca. CAPAN 2 | 0.0 | Renal ca. A498 | 1.4 |
| Adrenal gland | 19.6 | Renal ca. RXF 393 | 3.4 |
| Thyroid | 16.3 | Renal ca. ACHN | 1.4 |
| Salivary gland | 0.0 | Renal ca. UO-31 | 2.8 |
| Pituitary gland | 1.9 | Renal ca. TK-10 | 4.4 |

| | | | |
|------------------|-----|----------------------------------|-----|
| Brain (amygdala) | 6.7 | Liver ca. (hepatoblast) HepG2 | 0.0 |
|------------------|-----|----------------------------------|-----|

| | | | |
|--------------------------|------|-----------------------------------|-------|
| Brain (cerebellum) | 1.6 | Lung | 8.8 |
| Brain (hippocampus) | 22.2 | Lung (fetal) | 1.7 |
| Brain (substantia nigra) | 3.1 | Lung ca. (small cell) LX-1 | 18.6 |
| Brain (thalamus) | 3.2 | Lung ca. (small cell) NCI-H69 | 4.2 |
| Cerebral Cortex | 26.2 | Lung ca. (s.cell var.) SHP-77 | 100.0 |
| Spinal cord | 3.1 | Lung ca. (large cell)NCI-H460 | 0.0 |
| glio/astro U87-MG | 7.5 | Lung ca. (non-sm. cell) A549 | 6.7 |
| glio/astro U-118-MG | 4.2 | Lung ca. (non-s.cell) NCI-H23 | 5.7 |
| astrocytoma SW1783 | 1.2 | Lung ca. (non-s.cell) HOP-62 | 0.0 |
| neuro*; met SK-N-AS | 0.0 | Lung ca. (non-s.cl) NCI-H522 | 0.0 |
| astrocytoma SF-539 | 0.0 | Lung ca. (squam.) SW 900 | 0.9 |
| astrocytoma SNB-75 | 4.3 | Lung ca. (squam.) NCI-H596 | 3.7 |
| glioma SNB-19 | 6.0 | Mammary gland | 6.3 |
| glioma U251 | 14.1 | Breast ca.* (pl.ef) MCF-7 | 0.0 |
| glioma SF-295 | 0.0 | Breast ca.* (pl.ef) MDA-MB-231 | 45.4 |
| Heart (fetal) | 1.4 | Breast ca.* (pl.ef) T47D | 4.3 |
| Heart | 1.0 | Breast ca. BT-549 | 7.1 |
| Skeletal muscle (fetal) | 0.7 | Breast ca. MDA-N | 0.0 |
| Skeletal muscle | 3.2 | Ovary | 10.9 |
| Bone marrow | 3.1 | Ovarian ca. OVCAR- 3 | 0.0 |
| Thymus | 5.7 | Ovarian ca. OVCAR- 4 | 2.4 |
| Spleen | 7.2 | Ovarian ca. OVCAR- 5 | 5.2 |
| Lymph node | 0.0 | Ovarian ca. OVCAR- 8 | 0.0 |
| | | Ovarian ca. IGROV- | |

Office:

| | | | | |
|-----------------|-----|-------|--------|-----|
| Small intestine | 1.5 | SK OV | Uterus | 5.8 |
|-----------------|-----|-------|--------|-----|

| | | | |
|-------------------------------------|------|---------------------------------|------|
| Colon ca. SW480 | 33.2 | Placenta | 0.0 |
| Colon ca.* SW620(SW480 met) | 8.8 | Prostate | 1.6 |
| Colon ca. HT29 | 0.0 | Prostate ca.* (bone met)PC-3 | 2.6 |
| Colon ca. HCT-116 | 0.0 | Testis | 7.4 |
| Colon ca. CaCo-2 | 35.4 | Melanoma Hs688(A).T | 0.0 |
| Colon ca. tissue(ODO3866) | 24.5 | Melanoma* (met) Hs688(B).T | 0.0 |
| Colon ca. HCC-2998 | 15.7 | Melanoma UACC-62 | 0.0 |
| Gastric ca.* (liver met) NCI-N87 | 6.4 | Melanoma M14 | 0.0 |
| Bladder | 14.6 | Melanoma LOX IMVI | 0.0 |
| Trachea | 4.4 | Melanoma* (met) SK-MEL-5 | 0.0 |
| Kidney | 2.4 | Adipose | 17.3 |

General_screening_panel_v1.4 Summary: Ag3952 Highest expression of this gene is seen in the adrenal gland (CT=29). Thus, this gene product may be a treatment for Addison's disease and other adrenalopathies. This gene also has low levels of expression in adipose, heart, skeletal muscle, pituitary, thyroid, and pancreas. Therapeutic modulation of this gene product may be important for the diagnosis or treatment of endocrine or metabolic disease, including Types 1 and 2 diabetes, obesity and pancreatitis.

Expression of this gene is also seen in sample derived from colon, gastric, lung and breast cancers. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, gastric, lung and breast cancers.

Low but significant levels of expression are also seen for all regions of the CNS examined. Thus, this gene product may be useful for treatment of CNS disorders such as Alzheimer's disease, Parkinson's disease, stroke, epilepsy, schizophrenia and multiple sclerosis.

from breast and colon cancers. Overall, expression is consistent with expression seen in Panel

1.4. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, gastric, lung and breast cancers.

Among metabolic tissues, significant levels of expression are seen in adipose and the adrenal gland. Thus, this gene product may be useful for treatment of obesity, Addison's disease and other adrenalopathies.

In addition, this gene is expressed in the hippocampus, and cerebral cortex. Both these regions of the brain undergo degeneration in Alzheimer's disease. Thus, therapeutic modulation of the expression or function of this gene may be effective in the treatment of this disease or any other neurodegenerative disorders.

AC. CG57399-02: PHOSPHOLIPASE ADRAB-B PRECURSOR

Expression of gene CG57399-02 was assessed using the primer-probe set Ag3952, described in Table ACA. Results of the RTQ-PCR runs are shown in Table ACB. Please note that this gene represents a variant of CG57399-01. This sequence however, only corresponds to probe and primer set Ag3952.

Table ACA. Probe Name Ag3952

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-ctgtgtccctgtgtcctgaa-3' | 20 | 578 | 481 |
| Probe | TET-5'-tcaacagaacttgctaccctatcga-3' - TAMRA | 26 | 611 | 482 |
| Reverse | 5'-gtgggtcttctcctgaaacttc-3' | 22 | 646 | 483 |

Table ACB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3952, Run 213856126 | Tissue Name | Rel. Exp.(%) Ag3952, Run 213856126 |
|---------------|---------------------------------------|----------------------|---------------------------------------|
| Adipose | 9.0 | Renal ca. TK-10 | 15.0 |
| Melanoma* | 2.0 | Bladder | 22.7 |
| (18088(B)) | | (SC-1-NN) | |
| Melanoma* M14 | 0.9 | Gastric ca. KATO III | 75.3 |

| | | | |
|-------------------------------|------|-------------------------------------|------|
| Melanoma* LOXIMVI | 11.7 | Colon ca. SW-948 | 4.3 |
| Melanoma* SK-MEL-5 | 1.5 | Colon ca. SW480 | 97.3 |
| Squamous cell carcinoma SCC-4 | 8.7 | Colon ca.* (SW480 met) SW620 | 4.4 |
| Testis Pool | 12.8 | Colon ca. HT29 | 0.4 |
| Prostate ca.* (bone met) PC-3 | 10.5 | Colon ca. HCT-116 | 1.2 |
| Prostate Pool | 12.9 | Colon ca. CaCo-2 | 60.7 |
| Placenta | 5.1 | Colon cancer tissue | 28.7 |
| Uterus Pool | 6.5 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 7.3 | Colon ca. Colo-205 | 0.9 |
| Ovarian ca. SK-OV-3 | 26.4 | Colon ca. SW-48 | 26.1 |
| Ovarian ca. OVCAR-4 | 1.9 | Colon Pool | 18.8 |
| Ovarian ca. OVCAR-5 | 6.7 | Small Intestine Pool | 5.3 |
| Ovarian ca. IGROV-1 | 9.2 | Stomach Pool | 7.9 |
| Ovarian ca. OVCAR-8 | 4.2 | Bone Marrow Pool | 8.4 |
| Ovary | 10.0 | Fetal Heart | 1.2 |
| Breast ca. MCF-7 | 0.4 | Heart Pool | 5.7 |
| Breast ca. MDA-MB-231 | 92.0 | Lymph Node Pool | 32.1 |
| Breast ca. BT 549 | 5.5 | Fetal Skeletal Muscle | 1.2 |
| Breast ca. T47D | 2.5 | Skeletal Muscle Pool | 4.7 |
| Breast ca. MDA-N | 1.6 | Spleen Pool | 18.2 |
| Breast Pool | 19.6 | Thymus Pool | 19.3 |
| Trachea | 10.3 | CNS cancer (glio/astro) U87-MG | 38.2 |
| Lung | 1.2 | CNS cancer (glio/astro) U-118-MG | 12.2 |
| Fetal Lung | 8.3 | CNS cancer (neuro;met) SK-N-AS | 0.9 |
| Lung ca. NCI-N417 | 0.9 | CNS cancer (astro) SF-539 | 7.6 |

| Lung ca. NCI-N417 | SNB 19 |
|-------------------|--------|
| Lung ca. SHP-77 | 47.3 |

| | | | |
|-------------------|------|-------------------------------|-------|
| | | 295 | |
| Lung ca. A549 | 5.1 | Brain (Amygdala) Pool | 7.0 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 3.2 |
| Lung ca. NCI-H23 | 4.1 | Brain (fetal) | 19.3 |
| Lung ca. NCI-H460 | 0.5 | Brain (Hippocampus) Pool | 13.1 |
| Lung ca. HOP-62 | 2.7 | Cerebral Cortex Pool | 14.8 |
| Lung ca. NCI-H522 | 1.3 | Brain (Substantia nigra) Pool | 6.3 |
| Liver | 0.0 | Brain (Thalamus) Pool | 15.2 |
| Fetal Liver | 1.7 | Brain (whole) | 10.4 |
| Liver ca. HepG2 | 0.5 | Spinal Cord Pool | 5.3 |
| Kidney Pool | 21.2 | Adrenal Gland | 100.0 |
| Fetal Kidney | 1.6 | Pituitary gland Pool | 4.3 |
| Renal ca. 786-0 | 1.7 | Salivary Gland | 3.4 |
| Renal ca. A498 | 1.3 | Thyroid (female) | 14.5 |
| Renal ca. ACHN | 4.3 | Pancreatic ca. CAPAN2 | 1.7 |
| Renal ca. UO-31 | 17.4 | Pancreas Pool | 24.5 |

General_screening_panel_v1.4 Summary: Ag3952 Highest expression of this gene is seen in the adrenal gland (CT=29). Thus, this gene product may be a treatment for Addison's disease and other adrenalopathies. This gene also has low levels of expression in adipose, heart, skeletal muscle, pituitary, thyroid, and pancreas. Therapeutic modulation of this gene product may be important for the diagnosis or treatment of endocrine or metabolic disease, including Types 1 and 2 diabetes, obesity and pancreatitis.

Expression of this gene is also seen in cell line samples derived from colon, gastric, lung and breast cancers. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, gastric, lung and breast cancers.

Low but significant levels of expression are also seen for all regions of the CNS examined. Thus, this gene product may be useful for treatment of CNS disorders such as Alzheimer's disease, Parkinson's disease, stroke, epilepsy, schizophrenia and multiple

Expression of gene CG59311-01, splice variant CG59311-02, and full length clone CG59311-03, was assessed using the primer-probe set Ag3541, described in Table ADA. Results of the RTQ-PCR runs are shown in Tables ADB and ADC.

Table ADA. Probe Name Ag3541

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-ctcaactcaaaggcacaggtaga-3' | 22 | 1199 | 484 |
| Probe | TET-5'-tggcagcaaattcaaactttttcca-3' TAMRA | 26 | 1225 | 485 |
| Reverse | 5'-tttgctgtgcttgacagat-3' | 22 | 1269 | 486 |

Table ADB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3541, Run 217049294 | Tissue Name | Rel. Exp.(%) Ag3541, Run 217049294 |
|----------------------------------|------------------------------------|-------------------------------------|------------------------------------|
| Adipose | 0.0 | Renal ca. TK-10 | 6.0 |
| Melanoma* Hs688(A).T | 0.7 | Bladder | 3.7 |
| Melanoma* Hs688(B).T | 1.6 | Gastric ca. (liver met.) NCI-N87 | 0.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 0.0 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |
| Melanoma* SK-MEL-5 | 0.0 | Colon ca. SW480 | 2.7 |
| Squamous cell carcinoma SCC-4 | 0.0 | Colon ca.* (SW480 met) SW620 | 5.4 |
| Testis Pool | 3.1 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 1.4 | Colon ca. HCT-116 | 0.6 |
| Prostate Pool | 2.3 | Colon ca. CaCo-2 | 0.6 |
| Placenta | 0.5 | Colon cancer tissue | 0.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 2.9 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.0 | Colon ca. SW-48 | 0.0 |

| Variant ca. | Sample | Start Position |
|--------------------|--------|------------------|
| OVCAR-3 | | |
| Ovarian ca. IGROV- | 0.0 | Stomach Pool 3.1 |

| | | | |
|------------------------|------|-------------------------------------|--------------|
| 1 | | | |
| Ovarian ca. OVCAR-8 | 1.8 | Bone Marrow Pool | 1.4 |
| Ovary | 2.5 | Fetal Heart | 9.2 |
| Breast ca. MCF-7 | 2.4 | Heart Pool | 3.4 |
| Breast ca. MDA-MB-231 | 8.0 | Lymph Node Pool | 3.9 |
| Breast ca. BT 549 | 4.9 | Fetal Skeletal Muscle | 4.9 |
| Breast ca. T47D | 52.9 | Skeletal Muscle Pool | 13.5 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 0.0 |
| Breast Pool | 6.7 | Thymus Pool | 4.7 |
| Trachea | 0.9 | CNS cancer (glio/astro) U87-MG | 0.9 |
| Lung | 1.7 | CNS cancer (glio/astro) U-118-MG | 12.1 |
| Fetal Lung | 2.2 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 4.2 | CNS cancer (astro) SNB-75 | 5.2 |
| Lung ca. NCI-H146 | 2.1 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 6.7 | CNS cancer (glio) SF-295 | 0.7 |
| Lung ca. A549 | 0.0 | Brain (Amygdala) Pool | 4.2 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 100.0 |
| Lung ca. NCI-H23 | 10.2 | Brain (fetal) | 14.7 |
| Lung ca. NCI-H460 | 3.4 | Brain (Hippocampus) Pool | 9.0 |
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 9.7 |
| Lung ca. NCI-H522 | 8.5 | Brain (Substantia nigra) Pool | 3.5 |
| Liver | 0.5 | Brain (Thalamus) Pool | 10.5 |
| Fetal Liver | 1.5 | Brain (whole) | 12.9 |
| Liver ca. HepG2 | 0.5 | Spinal Cord Pool | 7.6 |
| Kidney Pool | 9.8 | Adrenal Gland | 10.2 |
| Fetal Kidney | 7.9 | Pituitary gland Pool | 3.1 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 1.7 |
| Reproductive 3.10% | 6.6 | Thyroid (female) | 0.0 |

| Tissue Name | Rel. Exp.(%) Ag3541, Run 166447041 | Tissue Name | Rel. Exp.(%) Ag3541, Run 166447041 |
|--------------------------------|--|---|--|
| Secondary Th1 act | 2.7 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 4.1 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 0.0 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 2.1 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 0.0 |
| Primary Th1 act | 2.7 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 0.0 |
| Primary Tr1 act | 0.0 | Microsvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 0.0 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 0.0 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 0.0 | Coronery artery SMC rest | 2.3 |
| CD45RO CD4 lymphocyte act | 1.7 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 1.8 |
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 0.0 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 4.2 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 1.4 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 0.0 |
| LAK cells rest | 2.8 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 9.8 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 22.2 |
| LAK cells IL-2+IL-12 | 0.0 | Lupus kidney | 18.4 |
| LAK cells IL-2+IFN | | | |

| | | | |
|---------------------------|-----|---------------|------|
| AK cells PMA/ionomycin | 0.0 | NCI-H292 IL-9 | 15.2 |
|---------------------------|-----|---------------|------|

| | | | |
|------------------------------|-----|---------------------------------------|--------------|
| NK Cells IL-2 rest | 1.7 | NCI-H292 IL-13 | 3.1 |
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 7.3 |
| Two Way MLR 5 day | 5.3 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 1.7 |
| PBMC PWM | 0.0 | Lung fibroblast TNF alpha + IL-1 beta | 5.7 |
| PBMC PHA-L | 2.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 0.0 |
| Ramos (B cell) ionomycin | 2.2 | Lung fibroblast IL-13 | 3.2 |
| B lymphocytes PWM | 0.0 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 rest | 2.9 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 2.9 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 3.5 | Dermal fibroblast IL-4 | 1.5 |
| Dendritic cells anti-CD40 | 0.0 | IBD Colitis 2 | 5.4 |
| Monocytes rest | 0.0 | IBD Crohn's | 0.0 |
| Monocytes LPS | 0.0 | Colon | 14.1 |
| Macrophages rest | 4.5 | Lung | 0.0 |
| Macrophages LPS | 2.1 | Thymus | 100.0 |
| HUVEC none | 0.0 | Kidney | 2.3 |
| HUVEC starved | 2.5 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3541 - Expression of this gene is low/undetectable (CTs > 34.5) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3541 Significant expression of this gene is seen only in cerebellum, fetal brain, the breast cancer cell line T47D, and ovarian cancer cell line OVCAR-5 (CTs=32-35). Therefore, expression of this gene can be used to differentiate

Panel 4D Summary: Ag3544 - Thymic epithelial expression (TIE) - Thymus (CT=33.8) (CT=33.8). Therefore, expression of this gene may be used to identify thymic tissue.

Furthermore, drugs that inhibit the function of this protein may regulate T cell development in the thymus and reduce or eliminate the symptoms of T cell mediated autoimmune or inflammatory diseases, including asthma, allergies, inflammatory bowel disease, lupus erythematosus, or rheumatoid arthritis. Additionally, therapeutics designed against this putative protein may disrupt T cell development in the thymus and function as an immunosuppressant for tissue transplant.

AE. CG59309-01: ACYL-COENZYME A THIOESTER HYDROLASE

Expression of gene CG59309-01 was assessed using the primer-probe set Ag3540, described in Table AEA. Results of the RTQ-PCR runs are shown in Tables AEB, AEC, AED and AEE.

Table AEA. Probe Name Ag3540

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-ccacgttggcttagcttatta-3' | 22 | 649 | 487 |
| Probe | TET-5'-tgaagatctcccaataacatggaca-3' - TAMRA | 26 | 677 | 488 |
| Reverse | 5'-ttcgaagtactccaggatatg-3' | 22 | 704 | 489 |

Table AEB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3540, Run 210638385 | Tissue Name | Rel. Exp.(%) Ag3540, Run 210638385 |
|------------------|---------------------------------------|----------------------------------|---------------------------------------|
| AD 1 Hippo | 13.7 | Control (Path) 3 Temporal Ctx | 8.2 |
| AD 2 Hippo | 26.2 | Control (Path) 4 Temporal Ctx | 34.2 |
| AD 3 Hippo | 13.1 | AD 1 Occipital Ctx | 23.2 |
| AD 4 Hippo | 3.4 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 hippo | 30.4 | AD 3 Occipital Ctx | 7.8 |
| AD 6 Hippo | 55.9 | AD 4 Occipital Ctx | 15.0 |
| Control 2 Hippo | 24.0 | AD 5 Occipital Ctx | 8.1 |
| Control 4 Hippo | 4.5 | AD 6 Occipital Ctx | 76.3 |
| Control (Path) 3 | | Control 1 Occipital | |

| Sample | Rel. Exp.(%) |
|---------------------|--------------|
| AD 2 Temporal Ctx | 19.5 |
| Control 3 Occipital | 36.3 |

| | | | |
|-------------------------------|------|--------------------------------|-------|
| | | Ctx | |
| AD 3 Temporal Ctx | 4.8 | Control 4 Occipital Ctx | 3.9 |
| AD 4 Temporal Ctx | 15.6 | Control (Path) 1 Occipital Ctx | 100.0 |
| AD 5 Inf Temporal Ctx | 36.9 | Control (Path) 2 Occipital Ctx | 7.6 |
| AD 5 SupTemporal Ctx | 27.4 | Control (Path) 3 Occipital Ctx | 1.6 |
| AD 6 Inf Temporal Ctx | 47.3 | Control (Path) 4 Occipital Ctx | 16.6 |
| AD 6 Sup Temporal Ctx | 64.2 | Control 1 Parietal Ctx | 8.7 |
| Control 1 Temporal Ctx | 7.0 | Control 2 Parietal Ctx | 20.7 |
| Control 2 Temporal Ctx | 53.2 | Control 3 Parietal Ctx | 27.2 |
| Control 3 Temporal Ctx | 19.9 | Control (Path) 1 Parietal Ctx | 88.9 |
| Control 4 Temporal Ctx | 10.5 | Control (Path) 2 Parietal Ctx | 10.8 |
| Control (Path) 1 Temporal Ctx | 68.3 | Control (Path) 3 Parietal Ctx | 10.1 |
| Control (Path) 2 Temporal Ctx | 25.3 | Control (Path) 4 Parietal Ctx | 47.6 |

Table AEC_General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3540, Run 217049291 | Tissue Name | Rel. Exp.(%) Ag3540, Run 217049291 |
|-------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 1.3 | Renal ca. TK-10 | 0.1 |
| Melanoma* Hs688(A).T | 0.7 | Bladder | 1.1 |
| Melanoma* Hs688(B).T | 0.5 | Gastric ca. (liver met.) NCI-N87 | 5.6 |
| Melanoma* M14 | 0.2 | Gastric ca. KATO III | 0.0 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |
| Melanoma* SK-MEL-5 | 0.0 | Colon ca. SW480 | 10.3 |
| Squamous cell | | Colon ca * (SW480) | |

| | | | |
|----------------------------------|-----|-------------------|-----|
| Prostate ca * (bone met) PC-3 | 0.8 | Colon ca. HCT-116 | 0.0 |
|----------------------------------|-----|-------------------|-----|

| | | | |
|------------------------|-------|-------------------------------------|-----|
| Prostate Pool | 0.3 | Colon ca. CaCo-2 | 3.5 |
| Placenta | 1.4 | Colon cancer tissue | 1.4 |
| Uterus Pool | 0.1 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 1.6 | Colon ca. Colo-205 | 3.3 |
| Ovarian ca. SK-OV-3 | 3.6 | Colon ca. SW-48 | 1.7 |
| Ovarian ca. OVCAR-4 | 0.4 | Colon Pool | 0.2 |
| Ovarian ca. OVCAR-5 | 23.7 | Small Intestine Pool | 0.3 |
| Ovarian ca. IGROV-1 | 0.0 | Stomach Pool | 0.1 |
| Ovarian ca. OVCAR-8 | 0.0 | Bone Marrow Pool | 0.2 |
| Ovary | 0.1 | Fetal Heart | 0.4 |
| Breast ca. MCF-7 | 0.0 | Heart Pool | 0.2 |
| Breast ca. MDA-MB-231 | 2.5 | Lymph Node Pool | 0.3 |
| Breast ca. BT 549 | 3.0 | Fetal Skeletal Muscle | 0.1 |
| Breast ca. T47D | 100.0 | Skeletal Muscle Pool | 0.4 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 0.2 |
| Breast Pool | 0.3 | Thymus Pool | 0.3 |
| Trachea | 0.4 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.3 |
| Fetal Lung | 0.2 | CNS cancer (neuro;met) SK-N-AS | 1.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.6 |
| Lung ca. LX-1 | 3.5 | CNS cancer (astro) SNB-75 | 3.1 |
| Lung ca. NCI-H146 | 0.0 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 0.1 | CNS cancer (glio) SF-295 | 0.2 |
| Lung ca. A549 | 1.4 | Brain (Amygdala) Pool | 0.7 |
| Lung ca. NCI-H526 | 0.7 | Brain (cerebellum) | 2.1 |
| Lung ca. NCI-H23 | 1.3 | Brain (fetal) | 0.5 |

| | | Region | |
|-------------------|-----|--------------------------|-----|
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) | 1.3 |

| | | Pool | |
|-----------------|-----|-----------------------|-----|
| Liver | 2.6 | Brain (Thalamus) Pool | 1.1 |
| Fetal Liver | 0.8 | Brain (whole) | 1.4 |
| Liver ca. HepG2 | 0.1 | Spinal Cord Pool | 0.5 |
| Kidney Pool | 0.7 | Adrenal Gland | 0.8 |
| Fetal Kidney | 0.6 | Pituitary gland Pool | 0.1 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 0.2 |
| Renal ca. A498 | 0.0 | Thyroid (female) | 0.7 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 9.4 |
| Renal ca. UO-31 | 1.1 | Pancreas Pool | 0.9 |

Table AED. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3540, Run 166447040 | Tissue Name | Rel. Exp.(%) Ag3540, Run 166447040 |
|---------------------------|---|---|---|
| Secondary Th1 act | 4.8 | HUVEC IL-1beta | 1.7 |
| Secondary Th2 act | 10.2 | HUVEC IFN gamma | 0.9 |
| Secondary Tr1 act | 12.9 | HUVEC TNF alpha + IFN gamma | 1.5 |
| Secondary Th1 rest | 2.1 | HUVEC TNF alpha + IL4 | 0.8 |
| Secondary Th2 rest | 1.4 | HUVEC IL-11 | 1.5 |
| Secondary Tr1 rest | 1.6 | Lung Microvascular EC none | 0.6 |
| Primary Th1 act | 4.7 | Lung Microvascular EC TNFalpha + IL-1beta | 0.8 |
| Primary Th2 act | 6.8 | Microvascular Dermal EC none | 1.5 |
| Primary Tr1 act | 7.3 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.8 |
| Primary Th1 rest | 6.6 | Bronchial epithelium TNFalpha + IL1beta | 1.3 |
| Primary Th2 rest | 2.6 | Small airway epithelium none | 0.6 |
| Primary Tr1 rest | 4.2 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 4.1 | Coronery artery SMC rest | 0.9 |
| CD45RO CD4 lymphocyte act | 10.9 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |

| Lymphocyte rest | IL-1beta |
|-----------------|----------|
| Secondary CD8 | 6.0 |

| | | | |
|------------------------------------|------|--|------|
| lymphocyte act | | | |
| CD4 lymphocyte none | 2.0 | KU-812 (Basophil) PMA/ionomycin | 10.2 |
| 2ry Th1/Th2/Tr1_anti- CD95 CH11 | 2.4 | CCD1106 (Keratinocytes) none | 6.8 |
| LAK cells rest | 2.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 25.7 |
| LAK cells IL-2 | 16.2 | Liver cirrhosis | 12.0 |
| LAK cells IL-2+IL-12 | 12.8 | Lupus kidney | 5.1 |
| LAK cells IL-2+IFN gamma | 15.6 | NCI-H292 none | 44.8 |
| LAK cells IL-2+ IL-18 | 7.4 | NCI-H292 IL-4 | 37.6 |
| LAK cells PMA/ionomycin | 3.4 | NCI-H292 IL-9 | 41.2 |
| NK Cells IL-2 rest | 9.0 | NCI-H292 IL-13 | 19.8 |
| Two Way MLR 3 day | 10.5 | NCI-H292 IFN gamma | 30.1 |
| Two Way MLR 5 day | 7.2 | HPAEC none | 1.2 |
| Two Way MLR 7 day | 8.9 | HPAEC TNF alpha + IL-1 beta | 3.3 |
| PBMC rest | 0.5 | Lung fibroblast none | 0.9 |
| PBMC PWM | 3.8 | Lung fibroblast TNF alpha + IL-1 beta | 0.7 |
| PBMC PHA-L | 1.0 | Lung fibroblast IL-4 | 0.5 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 0.0 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 0.9 |
| B lymphocytes PWM | 10.3 | Lung fibroblast IFN gamma | 1.2 |
| B lymphocytes CD40L and IL-4 | 3.8 | Dermal fibroblast CCD1070 rest | 1.1 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 18.9 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 1.9 |
| Dendritic cells none | 14.9 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 8.9 | Dermal fibroblast IL-4 | 1.5 |
| Dendritic cells anti- CD40 | 7.9 | IBD Colitis 2 | 2.9 |
| Monocytes rest | 0.0 | IBD Crohn's | 1.9 |

| Macrophages / PS | Thymus | 100,0 | |
|------------------|--------|--------|-----|
| HUVEC none | 1.1 | Kidney | 1.8 |

| | | | |
|---------------|-----|--|--|
| HUVEC starved | 1.4 | | |
|---------------|-----|--|--|

Table AEE. Panel 5 Islet

| Tissue Name | Rel. Exp.(%) Ag3540, Run 242386396 | Tissue Name | Rel. Exp.(%) Ag3540, Run 242386396 |
|------------------------------------|--|---|--|
| 97457_Patient-02go_adipose | 3.3 | 94709_Donor 2 AM - A_adipose | 9.1 |
| 97476_Patient-07sk_skeletal muscle | 0.8 | 94710_Donor 2 AM - B_adipose | 1.6 |
| 97477_Patient-07ut_uterus | 0.0 | 94711_Donor 2 AM - C_adipose | 1.4 |
| 97478_Patient-07pl_placenta | 12.9 | 94712_Donor 2 AD - A_adipose | 2.8 |
| 99167_Bayer Patient 1 | 15.5 | 94713_Donor 2 AD - B_adipose | 5.8 |
| 97482_Patient-08ut_uterus | 3.4 | 94714_Donor 2 AD - C_adipose | 4.2 |
| 97483_Patient-08pl_placenta | 3.4 | 94742_Donor 3 U - A_Mesenchymal Stem Cells | 3.0 |
| 97486_Patient-09sk_skeletal muscle | 100.0 | 94743_Donor 3 U - B_Mesenchymal Stem Cells | 1.1 |
| 97487_Patient-09ut_uterus | 1.6 | 94730_Donor 3 AM - A_adipose | 4.3 |
| 97488_Patient-09pl_placenta | 2.6 | 94731_Donor 3 AM - B_adipose | 2.0 |
| 97492_Patient-10ut_uterus | 3.1 | 94732_Donor 3 AM - C_adipose | 2.0 |
| 97493_Patient-10pl_placenta | 23.2 | 94733_Donor 3 AD - A_adipose | 10.7 |
| 97495_Patient-11go_adipose | 0.8 | 94734_Donor 3 AD - B_adipose | 3.0 |
| 97496_Patient-11sk_skeletal muscle | 0.0 | 94735_Donor 3 AD - C_adipose | 4.0 |
| 97497_Patient-11ut_uterus | 2.5 | 77138_Liver_HepG2untreated | 0.7 |
| 97498_Patient-11pl_placenta | 6.7 | 73556_Heart_Cardiac stromal cells (primary) | 0.0 |
| 97500_Patient-12go_adipose | 6.5 | 81735_Small Intestine | 4.8 |
| 97501_Patient- | . | 72409_Kidney_Proximal | . |

| | | | |
|----------------|-----|------------------------------|-----|
| Pat uteru | | | |
| 97503_Patient- | 2.4 | 90650_Adrenal_Adrenocortical | 0.6 |

| | | | |
|--|-----|--|-----|
| 12pl_placenta | | adenoma | |
| 94721_Donor 2 U - A_Mesenchymal Stem Cells | 2.2 | 72410_Kidney_HRCE | 8.0 |
| 94722_Donor 2 U - B_Mesenchymal Stem Cells | 0.6 | 72411_Kidney_HRE | 8.5 |
| 94723_Donor 2 U - C_Mesenchymal Stem Cells | 3.1 | 73139_Uterus_Uterine smooth muscle cells | 0.0 |

CNS_neurodegeneration_v1.0 Summary: Ag3540 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment.

General_screening_panel_v1.4 Summary: Ag3540 This gene is most highly expressed in a breast cancer cell line (CT=27.1). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of breast cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of breast cancer.

Among metabolic tissues, this gene, an acyl coA thioesterase homolog, has a low level of expression in adipose, adult and fetal liver, adrenal, thyroid and pancreas. Acyl CoA thioesterases have multiple roles in lipid homeostasis. Therefore, therapeutic modulation of this gene product may be a treatment for endocrine and metabolic disease, including Types 1 and 2 diabetes and obesity.

In addition, this gene is expressed in all CNS regions examined. Thus, therapeutic modulation of the expression or function of this gene may be effective in the treatment of neurologic disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, stroke, schizophrenia and multiple sclerosis.

References:

2. Hunt MC, Nousiainen SE, Huttunen MK, Orii KE, Svensson LT, Alexson SE. Peroxisome proliferator-induced long chain acyl-CoA thioesterases comprise a highly conserved novel multi-gene family involved in lipid metabolism. *J Biol Chem.* 1999 Nov 26;274(48):34317-26.

Panel 4D Summary: Ag3540 Highest expression of the CG59309-01 gene is seen in the thymus and colon (CTs=31.5). Significant levels of expression are also seen in a cluster of treated and untreated samples derived from the NCI-H292 mucoepidermoid cell line. Thus, expression of this gene could be used as a marker for thymus and colon. Furthermore, therapeutic modulation of the expression or function of this gene may regulate T cell development in the thymus and reduce or eliminate the symptoms of T cell mediated autoimmune or inflammatory diseases, including asthma, allergies, inflammatory bowel disease, lupus erythematosus, or rheumatoid arthritis. Additionally, small molecule or antibody therapeutics designed against this putative protein may disrupt T cell development in the thymus and function as an immunosuppressant for tissue transplant.

Panel 5 Islet Summary: Ag3540 This gene has moderate expression in skeletal muscle, (highest expression CT=30.5). Acyl CoA thioesterases function in peroxisomal fatty acid oxidation. Therefore, therapeutic modulation of this homolog may increase fatty acid oxidation in muscle and be a treatment for Type 2 diabetes and obesity.

References:

1. Hunt MC, Solaas K, Kase BF, Alexson SE. Characterization of an acyl-coA thioesterase that functions as a major regulator of peroxisomal lipid metabolism. *J Biol Chem.* 2002 Jan 11;277(2):1128-38.

AF. CG57364-01: CG6896

Expression of gene CG57364-01 was assessed using the primer-probe sets Ag3218 and Ag3378, described in Tables AFA and AFB. Results of the RTQ-PCR runs are shown in Tables AFC, AFD, AFE and AFF.

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|-----------|--------|----------------|------------|
|---------|-----------|--------|----------------|------------|

| | | | | |
|---------|---|----|-----|-----|
| Forward | 5'-ctcctgaagcaggctctt-3' | 20 | 249 | 490 |
| Probe | TET-5'-cctcccagtgtgccttcggagg-3' - TAMRA | 25 | 270 | 491 |
| Reverse | 5'-gacttctccaggcatttcg-3' | 21 | 303 | 492 |

Table AFB. Probe Name Ag3378

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-ctcctgaagcaggctctt-3' | 20 | 249 | 493 |
| Probe | TET-5'-cctcccagtgtgccttcggagg-3' - TAMRA | 25 | 270 | 494 |
| Reverse | 5'-gacttctccaggcatttcg-3' | 21 | 303 | 495 |

Table AFC. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3218, Run 209861784 | Rel. Exp.(%) Ag3378, Run 210154573 | Tissue Name | Rel. Exp.(%) Ag3218, Run 209861784 | Rel. Exp.(%) Ag3378, Run 210154573 |
|--------------------|--|--|--|--|--|
| AD 1 Hippo | 37.6 | 30.4 | Control (Path) 3 Temporal Ctx | 17.6 | 16.7 |
| AD 2 Hippo | 31.0 | 37.6 | Control (Path) 4 Temporal Ctx | 37.6 | 31.2 |
| AD 3 Hippo | 34.2 | 21.5 | AD 1 Occipital Ctx | 56.3 | 40.3 |
| AD 4 Hippo | 40.6 | 25.3 | AD 2 Occipital Ctx (Missing) | 0.0 | 0.0 |
| AD 5 hippo | 100.0 | 69.3 | AD 3 Occipital Ctx | 43.2 | 24.1 |
| AD 6 Hippo | 62.9 | 55.9 | AD 4 Occipital Ctx | 80.1 | 24.3 |
| Control 2 Hippo | 55.1 | 52.9 | AD 5 Occipital | 17.9 | 25.2 |

| Hippo | Occipital Ctx |
|-------|------------------|
| | |

| | | | | | |
|-------------------------------|------|--------------|--------------------------------|------|------|
| Control (Path) 3 Hippo | 22.8 | 26.8 | Control 1 Occipital Ctx | 27.9 | 17.4 |
| AD 1 Temporal Ctx | 40.3 | 28.3 | Control 2 Occipital Ctx | 94.0 | 64.6 |
| AD 2 Temporal Ctx | 83.5 | 94.6 | Control 3 Occipital Ctx | 43.5 | 40.6 |
| AD 3 Temporal Ctx | 30.8 | 24.5 | Control 4 Occipital Ctx | 20.3 | 22.5 |
| AD 4 Temporal Ctx | 61.1 | 26.8 | Control (Path) 1 Occipital Ctx | 79.6 | 51.4 |
| AD 5 Inf Temporal Ctx | 84.7 | 100.0 | Control (Path) 2 Occipital Ctx | 34.4 | 24.7 |
| AD 5 SupTemporal Ctx | 55.9 | 39.8 | Control (Path) 3 Occipital Ctx | 25.2 | 16.2 |
| AD 6 Inf Temporal Ctx | 47.0 | 46.0 | Control (Path) 4 Occipital Ctx | 76.3 | 45.1 |
| AD 6 Sup Temporal Ctx | 63.7 | 41.2 | Control 1 Parietal Ctx | 31.0 | 21.9 |
| Control 1 Temporal Ctx | 32.8 | 18.0 | Control 2 Parietal Ctx | 67.4 | 45.1 |
| Control 2 Temporal Ctx | 52.1 | 39.2 | Control 3 Parietal Ctx | 31.4 | 29.3 |
| Control 3 Temporal Ctx | 34.9 | 28.1 | Control (Path) 1 Parietal Ctx | 48.6 | 58.6 |
| Control 4 Temporal Ctx | 62.9 | 36.3 | Control (Path) 2 Parietal Ctx | 46.3 | 27.0 |
| Control (Path) 1 Temporal Ctx | 75.8 | 50.0 | Control (Path) 3 Parietal Ctx | 26.1 | 23.8 |

Table AFD. Panel 1.3D

| Tissue Name | Rel. Exp.(%) Ag3218, Run 168013878 | Rel. Exp.(%) Ag3378, Run 165674263 | Tissue Name | Rel. Exp.(%) Ag3218, Run 168013878 | Rel. Exp.(%) Ag3378, Run 165674263 |
|---------------------------|--|--|-------------------------------------|--|--|
| Liver adenocarcinoma | 10.7 | 20.2 | Kidney (fetal) | 48.3 | 13.9 |
| Pancreas | 10.8 | 13.1 | Renal ca. 786-0 | 15.6 | 10.4 |
| Pancreatic ca. CAPAN 2 | 9.6 | 5.4 | Renal ca. A498 | 19.2 | 14.9 |
| Adrenal gland | 5.1 | 18.4 | Renal ca. RXF 393 | 39.0 | 33.2 |
| Thyroid | 12.3 | 33.2 | Renal ca. ACHN | 12.1 | 11.3 |
| Salivary gland | 5.1 | 5.5 | Renal ca. UO-31 | 18.9 | 17.8 |
| Pituitary gland | 21.5 | 74.7 | Renal ca. TK-10 | 20.0 | 10.1 |
| Brain (fetal) | 19.5 | 36.1 | Liver | 18.0 | 8.7 |
| Brain (whole) | 22.1 | 29.9 | Liver (fetal) | 5.5 | 25.3 |
| Brain (amygdala) | 57.4 | 46.7 | Liver ca. (hepatoblast) HepG2 | 14.2 | 14.1 |
| Brain (cerebellum) | 25.2 | 23.5 | Lung | 14.1 | 18.7 |
| Brain (hippocampus) | 28.1 | 85.9 | Lung (fetal) | 17.2 | 4.0 |
| Brain (substantia nigra) | 11.5 | 16.7 | Lung ca. (small cell) LX-1 | 6.5 | 14.8 |
| Brain (thalamus) | 57.0 | 67.4 | Lung ca. (small cell) NCI-H69 | 20.6 | 4.8 |
| Cerebral Cortex | 75.8 | 36.9 | Lung ca. (s.cell var.) SHP-77 | 100.0 | 39.8 |
| Spinal cord | 9.7 | 13.2 | Lung ca. (large cell) NCI-H460 | 5.0 | 37.1 |
| glio/astro U87-MG | 22.8 | 13.6 | Lung ca. (non-sm. cell) A549 | 27.7 | 13.6 |
| glio/astro U-118 | | | Lung ca. (non- | | |

| astrocytoma SW 1783 | glioblastoma U-118 | colorectal cancer (s.cell) HOP 62 |
|------------------------|-----------------------|--------------------------------------|
| neuro*, met SK-N-17.1 | 52.5 | Lung ca. (non-11.3 |

| AS | | | s.cl) NCI-H522 | | |
|-----------------------------------|------|------|-----------------------------------|------|------|
| astrocytoma SF-539 | 15.5 | 16.0 | Lung ca. (squam.) SW 900 | 23.2 | 13.5 |
| astrocytoma SNB-75 | 43.8 | 50.0 | Lung ca. (squam.) NCI-H596 | 41.5 | 10.2 |
| glioma SNB-19 | 17.9 | 26.2 | Mammary gland | 14.8 | 35.1 |
| glioma U251 | 47.6 | 39.0 | Breast ca.* (pl.ef) MCF-7 | 48.6 | 39.0 |
| glioma SF-295 | 12.3 | 10.7 | Breast ca.* (pl.ef) MDA-MB-231 | 25.9 | 60.7 |
| Heart (fetal) | 38.4 | 8.0 | Breast ca.* (pl.ef) T47D | 77.4 | 21.2 |
| Heart | 3.5 | 5.0 | Breast ca. BT-549 | 47.0 | 95.9 |
| Skeletal muscle (fetal) | 17.0 | 10.0 | Breast ca. MDA-N | 16.6 | 7.3 |
| Skeletal muscle | 4.4 | 7.2 | Ovary | 10.1 | 4.7 |
| Bone marrow | 1.3 | 14.7 | Ovarian ca. OVCAR-3 | 36.3 | 31.2 |
| Thymus | 13.9 | 12.3 | Ovarian ca. OVCAR-4 | 33.0 | 20.7 |
| Spleen | 2.6 | 12.9 | Ovarian ca. OVCAR-5 | 42.6 | 15.7 |
| Lymph node | 1.7 | 15.9 | Ovarian ca. OVCAR-8 | 8.7 | 5.2 |
| Colorectal | 18.2 | 11.8 | Ovarian ca. IGROV-1 | 11.3 | 15.1 |
| Stomach | 14.8 | 33.7 | Ovarian ca.* (ascites) SK-OV-3 | 43.5 | 17.0 |
| Small intestine | 18.3 | 66.0 | Uterus | 10.5 | 21.8 |
| Colon ca. SW480 | 12.9 | 14.2 | Placenta | 2.6 | 15.0 |
| Colon ca.* SW620(SW480 met) | 17.0 | 14.2 | Prostate | 11.7 | 30.6 |
| Colon ca. HT29 | 17.2 | 18.8 | Prostate ca.* (bone met)PC | 35.4 | 40.3 |

| | | | | | |
|------------------|------|-----|----------|-----|-----|
| Colon ca. CaCo-2 | 20.9 | 7.4 | Melanoma | 5.0 | 1.4 |
|------------------|------|-----|----------|-----|-----|

| | | | | | |
|-------------------------------------|------|------|----------------------------------|------|------|
| | | | Hs688(A).T | | |
| Colon ca. tissue(ODO3866) | 14.7 | 21.9 | Melanoma* (met) Hs688(B).T | 6.0 | 3.5 |
| Colon ca. HCC- 2998 | 22.1 | 13.1 | Melanoma UACC-62 | 14.3 | 12.2 |
| Gastric ca.* (liver met) NCI-N87 | 48.6 | 82.4 | Melanoma M14 | 3.1 | 8.2 |
| Bladder | 6.2 | 4.7 | Melanoma LOX IMVI | 30.1 | 8.4 |
| Trachea | 12.8 | 49.3 | Melanoma* (met) SK- MEL-5 | 21.8 | 13.1 |
| Kidney | 43.5 | 35.4 | Adipose | 9.2 | 3.0 |

Table AFE. Panel 2.2

| Tissue Name | Rel. Exp.(%) Ag3218, Run 174416494 | Tissue Name | Rel. Exp.(%) Ag3218, Run 174416494 |
|--------------------------------------|--|---|--|
| Normal Colon | 5.9 | Kidney Margin (OD04348) | 70.2 |
| Colon cancer (OD06064) | 5.6 | Kidney malignant cancer (OD06204B) | 3.9 |
| Colon Margin (OD06064) | 3.6 | Kidney normal adjacent tissue (OD06204E) | 6.7 |
| Colon cancer (OD06159) | 6.3 | Kidney Cancer (OD04450-01) | 15.1 |
| Colon Margin (OD06159) | 7.0 | Kidney Margin (OD04450-03) | 3.1 |
| Colon cancer (OD06297-04) | 2.6 | Kidney Cancer 8120613 | 2.5 |
| Colon Margin (OD06297-05) | 5.6 | Kidney Margin 8120614 | 18.2 |
| CC Gr.2 ascend colon (ODO3921) | 20.0 | Kidney Cancer 9010320 | 2.4 |
| CC Margin (ODO3921) | 13.7 | Kidney Margin 9010321 | 4.4 |
| Colon cancer metastasis (OD06104) | 0.0 | Kidney Cancer 8120607 | 23.0 |
| Lung Margin | 11.0 | Kidney Margin | 15.1 |

| | | | |
|-------------|-----|-----------------------|-----|
| Lung Margin | 0.5 | Uterine Cancer 064011 | 0.1 |
|-------------|-----|-----------------------|-----|

| | | | |
|--|------|--|-------|
| (OD04451-02) | | | |
| Normal Prostate | 5.6 | Normal Thyroid | 6.6 |
| Prostate Cancer (OD04410) | 3.9 | Thyroid Cancer 064010 | 6.8 |
| Prostate Margin (OD04410) | 6.1 | Thyroid Cancer A302152 | 11.9 |
| Normal Ovary | 7.0 | Thyroid Margin A302153 | 7.7 |
| Ovarian cancer (OD06283-03) | 1.3 | Normal Breast | 3.4 |
| Ovarian Margin (OD06283-07) | 0.0 | Breast Cancer (OD04566) | 9.9 |
| Ovarian Cancer 064008 | 31.2 | Breast Cancer 1024 | 16.8 |
| Ovarian cancer (OD06145) | 3.5 | Breast Cancer (OD04590-01) | 100.0 |
| Ovarian Margin (OD06145) | 8.4 | Breast Cancer Mets (OD04590-03) | 26.2 |
| Ovarian cancer (OD06455-03) | 13.7 | Breast Cancer Metastasis (OD04655-05) | 36.3 |
| Ovarian Margin (OD06455-07) | 1.1 | Breast Cancer 064006 | 5.4 |
| Normal Lung | 5.4 | Breast Cancer 9100266 | 12.8 |
| Invasive poor diff. lung adeno (ODO4945-01) | 14.5 | Breast Margin 9100265 | 1.0 |
| Lung Margin (ODO4945-03) | 2.7 | Breast Cancer A209073 | 3.3 |
| Lung Malignant Cancer (OD03126) | 1.8 | Breast Margin A2090734 | 11.7 |
| Lung Margin (OD03126) | 5.1 | Breast cancer (OD06083) | 6.9 |
| Lung Cancer (OD05014A) | 12.8 | Breast cancer node metastasis (OD06083) | 10.7 |
| Lung Margin (OD05014B) | 3.3 | Normal Liver | 9.4 |
| Lung cancer (OD06081) | 6.3 | Liver Cancer 1026 | 2.6 |
| Lung Margin (OD06081) | 2.7 | Liver Cancer 1025 | 9.7 |
| Lung Cancer (OD04237-01) | 12.9 | Liver Cancer 6004-T | 10.4 |
| Lung Margin | 6.1 | Liver Tissue 6004-N | 5.2 |

| | | | |
|-----------------|-----|---------------------|------|
| Ocular Melanoma | 0.1 | Liver Tissue 6005-N | 11.2 |
|-----------------|-----|---------------------|------|

| | | | |
|---------------------------------------|------|------------------------|------|
| Margin (Liver) | | | |
| Melanoma Metastasis | 1.6 | Liver Cancer 064003 | 22.5 |
| Melanoma Margin (Lung) | 4.6 | Normal Bladder | 6.1 |
| Normal Kidney | 10.4 | Bladder Cancer 1023 | 10.8 |
| Kidney Ca, Nuclear grade 2 (OD04338) | 14.6 | Bladder Cancer A302173 | 15.1 |
| Kidney Margin (OD04338) | 10.5 | Normal Stomach | 15.0 |
| Kidney Ca Nuclear grade 1/2 (OD04339) | 44.8 | Gastric Cancer 9060397 | 7.1 |
| Kidney Margin (OD04339) | 17.7 | Stomach Margin 9060396 | 10.4 |
| Kidney Ca, Clear cell type (OD04340) | 5.3 | Gastric Cancer 9060395 | 8.4 |
| Kidney Margin (OD04340) | 25.3 | Stomach Margin 9060394 | 10.4 |
| Kidney Ca, Nuclear grade 3 (OD04348) | 7.5 | Gastric Cancer 064005 | 7.7 |

Table AFF. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3218, Run 164682519 | Rel. Exp.(%) Ag3378, Run 165296553 | Tissue Name | Rel. Exp.(%) Ag3218, Run 164682519 | Rel. Exp.(%) Ag3378, Run 165296553 |
|--------------------|---|---|-----------------------------|---|---|
| Secondary Th1 act | 18.2 | 25.7 | HUVEC IL-1beta | 14.5 | 12.9 |
| Secondary Th2 act | 39.0 | 26.6 | HUVEC IFN gamma | 47.0 | 25.3 |
| Secondary Tr1 act | 33.2 | 19.1 | HUVEC TNF alpha + IFN gamma | 43.5 | 45.1 |
| Secondary Th1 rest | 9.5 | 12.2 | HUVEC TNF alpha + IL4 | 37.1 | 48.0 |
| Secondary Th2 rest | 11.2 | 5.1 | HUVEC IL-11 | 43.5 | 18.0 |
| Secondary Tr1 rest | 22.7 | 8.0 | Lung Microvascular EC none | 16.8 | 61.6 |
| Primary Th1 act | 43.2 | 27.9 | Lung Microvascular EC | 18.6 | 14.7 |

Primary Th1 act

Microvascular

Dermal EC none

| | | | | | |
|---------------------------------------|------|------|---|------|------|
| Primary Tr1 act | 24.7 | 14.4 | Microvasular Dermal EC TNFalpha + IL-1beta | 66.4 | 22.1 |
| Primary Th1 rest | 25.2 | 17.4 | Bronchial epithelium TNFalpha + IL1beta | 30.6 | 29.3 |
| Primary Th2 rest | 15.5 | 7.5 | Small airway epithelium none | 36.1 | 24.3 |
| Primary Tr1 rest | 21.3 | 6.7 | Small airway epithelium TNFalpha + IL-1beta | 76.3 | 62.9 |
| CD45RA CD4 lymphocyte act | 35.4 | 16.6 | Coronery artery SMC rest | 49.7 | 28.1 |
| CD45RO CD4 lymphocyte act | 27.9 | 25.9 | Coronery artery SMC TNFalpha + IL-1beta | 25.3 | 23.7 |
| CD8 lymphocyte act | 21.0 | 14.8 | Astrocytes rest | 22.2 | 31.2 |
| Secondary CD8 lymphocyte rest | 39.2 | 17.8 | Astrocytes TNFalpha + IL-1beta | 26.1 | 25.0 |
| Secondary CD8 lymphocyte act | 20.9 | 7.4 | KU-812 (Basophil) rest | 90.8 | 85.3 |
| CD4 lymphocyte none | 4.5 | 11.8 | KU-812 (Basophil) PMA/ionomycin | 87.1 | 72.2 |
| 2ry Th1/Th2/Tr1_anti- CD95 CH11 | 2.6 | 10.0 | CCD1106 (Keratinocytes) none | 36.6 | 36.9 |
| LAK cells rest | 11.7 | 12.3 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 33.4 | 20.4 |
| LAK cells IL-2 | 6.8 | 27.5 | Liver cirrhosis | 25.5 | 19.9 |
| LAK cells IL-2+IL-12 | 37.1 | 11.6 | Lupus kidney | 44.4 | 15.7 |
| LAK cells IL-2+IFN gamma | 20.7 | 19.1 | NCI-H292 none | 79.6 | 64.6 |
| LAK cells IL-2+ | 21.9 | 14.7 | NCI-H292 IL-4 | 85.3 | 96.6 |

| NK Cells IL-2 rest | 44.9 | 11.0 | NCI-H292 IL-4 | 98.8 | 29.1 |
|--------------------|------|------|---------------|------|------|
| Two Way MLR 3 | 23.7 | 11.0 | NCI-H292 IFN | 80.1 | 56.6 |

| day | | | gamma | | |
|------------------------------|------|------|---------------------------------------|------|-------|
| Two Way MLR 5 day | 12.5 | 6.1 | HPAEC none | 38.4 | 27.2 |
| Two Way MLR 7 day | 12.3 | 8.7 | HPAEC TNF alpha + IL-1 beta | 42.6 | 43.2 |
| PBMC rest | 6.0 | 5.7 | Lung fibroblast none | 31.2 | 21.3 |
| PBMC PWM | 40.3 | 27.7 | Lung fibroblast TNF alpha + IL-1 beta | 14.7 | 24.5 |
| PBMC PHA-L | 37.9 | 17.7 | Lung fibroblast IL-4 | 47.0 | 42.6 |
| Ramos (B cell) none | 11.7 | 14.9 | Lung fibroblast IL-9 | 49.3 | 30.6 |
| Ramos (B cell) ionomycin | 33.9 | 26.8 | Lung fibroblast IL-13 | 36.6 | 42.6 |
| B lymphocytes PWM | 33.7 | 40.9 | Lung fibroblast IFN gamma | 44.8 | 22.5 |
| B lymphocytes CD40L and IL-4 | 34.4 | 18.3 | Dermal fibroblast CCD1070 rest | 33.7 | 47.3 |
| EOL-1 dbcAMP | 50.0 | 28.1 | Dermal fibroblast CCD1070 TNF alpha | 47.3 | 33.2 |
| EOL-1 dbcAMP PMA/ionomycin | 44.1 | 32.1 | Dermal fibroblast CCD1070 IL-1 beta | 50.0 | 34.6 |
| Dendritic cells none | 33.9 | 19.6 | Dermal fibroblast IFN gamma | 24.0 | 34.4 |
| Dendritic cells LPS | 21.9 | 10.2 | Dermal fibroblast IL-4 | 24.3 | 32.8 |
| Dendritic cells anti-CD40 | 49.7 | 33.9 | IBD Colitis 2 | 6.0 | 11.7 |
| Monocytes rest | 10.7 | 10.3 | IBD Crohn's | 25.3 | 26.1 |
| Monocytes LPS | 30.6 | 9.3 | Colon | 70.7 | 100.0 |
| Macrophages rest | 41.2 | 33.7 | Lung | 64.6 | 17.7 |
| Macrophages LPS | 20.0 | 7.5 | Thymus | 80.7 | 56.3 |
| HUVEC none | 26.8 | 29.5 | Kidney | 26.4 | 41.5 |
| HUVEC starved | 26.2 | 37.6 | | | |

CNS_neurodegeneration_v1.0 Summary: Ag3218/Ag3378 - Two different experiments using probe/primer sets with the same sequence are in very good agreement. This panel

DEPENDENT UPON INDIVIDUALS (10 ALZHEIMER'S DISEASE AND 10 NON-DEMENTED CONTROLS)

detected between Alzheimer's diseased postmortem brains and those of non-demented controls

in this experiment. Please see Panel 1.3D for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

Panel 1.3D Summary: Ag3218/Ag3378 - Two different experiments using probe/primer sets with the same sequence are in good agreement. Highest expression is seen in testis and a lung cancer cell line (CTs=30-31). This panel confirms the expression of this gene at low levels in the brain. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene product is also expressed in adipose, pancreas, thyroid, pituitary, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Based on expression in this panel, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

Panel 2.2 Summary: Ag3218 - This gene is expressed at low to moderate levels in many samples on this panel, with the highest levels of expression in breast cancer sample OD04590-01 (CT=30.3). This gene is expressed in a cluster of breast cancer samples with no expression in normal breast (CT>35). Similarly, this gene is expressed in ovarian cancer samples at higher levels than the matched margin samples.

Interestingly, this gene is expressed at higher levels in kidney cancer margin samples than in the matched cancer samples.

This gene is homologous to a mouse myosin phosphatase targeting subunit (MYPT) which have been found to play a role in cell division. MYPT undergoes mitosis-specific phosphorylation which is reversed during cytokinesis.

1. Totsukawa G, Yamakita Y, Yamashiro S, Hosoya H, Hartshorne DJ, Matsumura F. Activation of myosin phosphatase targeting subunit by mitosis-specific phosphorylation. J Cell Biol 1999 Feb 22;144(4):735-44.

Panel 4D Summary: Ag3218/Ag3378 - Two different experiments using probe/primer sets with the same sequence are in very good agreement. Highest expression is seen in the colon and a mucoepidermoid cell line (CTs=30-32). This gene is expressed at low to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AG. CG59241-01: Amiloride-sensitive sodium channel

Expression of gene CG59241-01 was assessed using the primer-probe set Ag3407, described in Table AGA. Results of the RTQ-PCR runs are shown in Tables AGB, AGC and AGD.

Table AGA. Probe Name Ag3407

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -gtcacccctctgcaacactaatg-3' | 22 | 268 | 496 |
| Probe | TET-5' -ctgtcccagctcagctaccctgacct-3' - TAMRA | 26 | 298 | 497 |
| Reverse | 5' -tttcatccaggcccagcat-3' | 19 | 340 | 498 |

Table AGR. CNS neurodegeneration v1.0

| Tissue Name | KCL Exp. of Ag3407 Run 210349883 | Tissue Name | KCL Exp. of Ag3407 Run 210349883 |
|-------------|-------------------------------------|-------------|-------------------------------------|
|-------------|-------------------------------------|-------------|-------------------------------------|

| | | | |
|----------------------------------|-------|-----------------------------------|------|
| AD 1 Hippo | 18.4 | Control (Path) 3 Temporal Ctx | 4.1 |
| AD 2 Hippo | 29.7 | Control (Path) 4 Temporal Ctx | 40.3 |
| AD 3 Hippo | 18.3 | AD 1 Occipital Ctx | 36.9 |
| AD 4 Hippo | 5.4 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 hippo | 91.4 | AD 3 Occipital Ctx | 19.1 |
| AD 6 Hippo | 80.7 | AD 4 Occipital Ctx | 18.8 |
| Control 2 Hippo | 9.3 | AD 5 Occipital Ctx | 18.3 |
| Control 4 Hippo | 19.9 | AD 6 Occipital Ctx | 28.9 |
| Control (Path) 3 Hippo | 8.8 | Control 1 Occipital Ctx | 4.3 |
| AD 1 Temporal Ctx | 28.5 | Control 2 Occipital Ctx | 80.1 |
| AD 2 Temporal Ctx | 41.8 | Control 3 Occipital Ctx | 20.2 |
| AD 3 Temporal Ctx | 32.5 | Control 4 Occipital Ctx | 6.0 |
| AD 4 Temporal Ctx | 36.3 | Control (Path) 1 Occipital Ctx | 92.7 |
| AD 5 Inf Temporal Ctx | 100.0 | Control (Path) 2 Occipital Ctx | 25.3 |
| AD 5 Sup Temporal Ctx | 56.6 | Control (Path) 3 Occipital Ctx | 3.0 |
| AD 6 Inf Temporal Ctx | 82.4 | Control (Path) 4 Occipital Ctx | 41.2 |
| AD 6 Sup Temporal Ctx | 44.1 | Control 1 Parietal Ctx | 21.9 |
| Control 1 Temporal Ctx | 15.3 | Control 2 Parietal Ctx | 79.0 |
| Control 2 Temporal Ctx | 24.1 | Control 3 Parietal Ctx | 22.2 |
| Control 3 Temporal Ctx | 34.6 | Control (Path) 1 Parietal Ctx | 77.9 |
| Control 4 Temporal Ctx | 12.0 | Control (Path) 2 Parietal Ctx | 47.6 |
| Control (Path) 1 Temporal Ctx | 53.6 | Control (Path) 3 Parietal Ctx | 6.2 |
| Control (Path) 2 Temporal Ctx | 56.6 | Control (Path) 4 Parietal Ctx | 67.4 |

| Tissue Name | Rel. Exp.(%) Ag3407, | Tissue Name | Rel. Exp.(%) Ag3407, |
|-------------|----------------------|-------------|----------------------|
|-------------|----------------------|-------------|----------------------|

| | Run 216821458 | | Run 216821458 |
|-------------------------------|----------------------|-------------------------------------|----------------------|
| Adipose | 0.2 | Renal ca. TK-10 | 16.6 |
| Melanoma* Hs688(A).T | 2.3 | Bladder | 0.3 |
| Melanoma* Hs688(B).T | 0.4 | Gastric ca. (liver met.) NCI-N87 | 8.8 |
| Melanoma* M14 | 2.0 | Gastric ca. KATO III | 0.7 |
| Melanoma* LOXIMVI | 2.5 | Colon ca. SW-948 | 3.7 |
| Melanoma* SK-MEL-5 | 8.7 | Colon ca. SW480 | 14.1 |
| Squamous cell carcinoma SCC-4 | 1.2 | Colon ca.* (SW480 met) SW620 | 21.2 |
| Testis Pool | 0.4 | Colon ca. HT29 | 10.7 |
| Prostate ca.* (bone met) PC-3 | 4.4 | Colon ca. HCT-116 | 64.2 |
| Prostate Pool | 2.3 | Colon ca. CaCo-2 | 32.3 |
| Placenta | 0.5 | Colon cancer tissue | 13.2 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 12.5 |
| Ovarian ca. OVCAR-3 | 8.4 | Colon ca. Colo-205 | 0.3 |
| Ovarian ca. SK-OV-3 | 9.7 | Colon ca. SW-48 | 0.6 |
| Ovarian ca. OVCAR-4 | 1.6 | Colon Pool | 2.8 |
| Ovarian ca. OVCAR-5 | 18.9 | Small Intestine Pool | 4.5 |
| Ovarian ca. IGROV-1 | 4.9 | Stomach Pool | 1.4 |
| Ovarian ca. OVCAR-8 | 5.9 | Bone Marrow Pool | 1.8 |
| Ovary | 2.0 | Fetal Heart | 2.4 |
| Breast ca. MCF-7 | 16.7 | Heart Pool | 0.3 |
| Breast ca. MDA-MB-231 | 12.1 | Lymph Node Pool | 3.5 |
| Breast ca. BT 549 | 22.7 | Fetal Skeletal Muscle | 1.9 |
| Breast ca. T47D | 27.4 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 4.5 | Spleen Pool | 0.0 |
| Breast Pool | 2.9 | Thymus Pool | 2.1 |
| Fetal Lung | 0.0 | CNS cancer (glio/astro) | 0.0 |

| Fetal Lung | 10.8 | CNS cancer | 58.6 |
|------------|------|------------|------|

| | | | |
|-------------------|------|-------------------------------|--------------|
| | | (neuro;met) SK-N-AS | |
| Lung ca. NCI-N417 | 1.3 | CNS cancer (astro) SF-539 | 28.1 |
| Lung ca. LX-1 | 21.8 | CNS cancer (astro) SNB-75 | 24.7 |
| Lung ca. NCI-H146 | 5.4 | CNS cancer (glio) SNB-19 | 7.3 |
| Lung ca. SHP-77 | 11.7 | CNS cancer (glio) SF-295 | 4.8 |
| Lung ca. A549 | 8.0 | Brain (Amygdala) Pool | 3.9 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 36.1 |
| Lung ca. NCI-H23 | 7.4 | Brain (fetal) | 100.0 |
| Lung ca. NCI-H460 | 5.4 | Brain (Hippocampus) Pool | 5.6 |
| Lung ca. HOP-62 | 2.9 | Cerebral Cortex Pool | 5.6 |
| Lung ca. NCI-H522 | 8.5 | Brain (Substantia nigra) Pool | 7.1 |
| Liver | 0.0 | Brain (Thalamus) Pool | 11.3 |
| Fetal Liver | 0.0 | Brain (whole) | 13.4 |
| Liver ca. HepG2 | 0.8 | Spinal Cord Pool | 12.7 |
| Kidney Pool | 2.1 | Adrenal Gland | 0.0 |
| Fetal Kidney | 3.7 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 1.7 | Salivary Gland | 0.9 |
| Renal ca. A498 | 0.7 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 1.9 | Pancreatic ca. CAPAN2 | 2.3 |
| Renal ca. UO-31 | 0.2 | Pancreas Pool | 2.6 |

Table AGD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3407, Run 165296462 | Tissue Name | Rel. Exp.(%) Ag3407, Run 165296462 |
|--------------------|--|-----------------------------|--|
| Secondary Th1 act | 7.9 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 17.1 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 40.1 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 4.4 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 7.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 11.7 | Lung Microvascular EC | 0.0 |

| | | | |
|-----------------|------|---------------------------------|-----|
| Primary Th2 act | 69.3 | Microvascular Dermal EC none | 0.0 |
|-----------------|------|---------------------------------|-----|

| | | | |
|--------------------------------|------|--|------|
| Primary Tr1 act | 90.8 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 20.0 | Bronchial epithelium TNFalpha + IL1beta | 0.0 |
| Primary Th2 rest | 42.6 | Small airway epithelium none | 3.0 |
| Primary Tr1 rest | 52.5 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 2.8 | Coronery artery SMC rest | 3.6 |
| CD45RO CD4 lymphocyte act | 14.0 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 5.8 | Astrocytes rest | 11.6 |
| Secondary CD8 lymphocyte rest | 18.9 | Astrocytes TNFalpha + IL-1beta | 0.0 |
| Secondary CD8 lymphocyte act | 22.2 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.0 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 4.5 | CCD1106 (Keratinocytes) none | 2.7 |
| LAK cells rest | 3.3 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |
| LAK cells IL-2 | 4.0 | Liver cirrhosis | 13.5 |
| LAK cells IL-2+IL-12 | 5.7 | Lupus kidney | 4.1 |
| LAK cells IL-2+IFN gamma | 21.3 | NCI-H292 none | 9.0 |
| LAK cells IL-2+ IL-18 | 6.7 | NCI-H292 IL-4 | 14.8 |
| LAK cells PMA/ionomycin | 0.0 | NCI-H292 IL-9 | 3.5 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 0.0 |
| Two Way MLR 3 day | 5.0 | NCI-H292 IFN gamma | 5.5 |
| Two Way MLR 5 day | 2.3 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 8.2 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 2.8 |
| PBMC PWM | 21.3 | Lung fibroblast TNF alpha + IL-1 beta | 0.0 |
| PBMC PHA-L | 20.4 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 0.0 |

| | | | |
|---------------------|-------|-------------------|------|
| B lymphocytes PWM | 100.0 | gamma | |
| B lymphocytes CD40L | 19.8 | Dermal fibroblast | 34.4 |

| | | | |
|-------------------------------|-----|--|------|
| and IL-4 | | CCD1070 rest | |
| EOL-1 dbcAMP | 2.6 | Dermal fibroblast CCD1070 TNF alpha | 68.8 |
| EOL-1 dbcAMP PMA/ionomycin | 6.2 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 0.0 | Dermal fibroblast IL-4 | 14.1 |
| Dendritic cells anti- CD40 | 6.0 | IBD Colitis 2 | 0.0 |
| Monocytes rest | 0.0 | IBD Crohn's | 0.0 |
| Monocytes LPS | 6.5 | Colon | 42.3 |
| Macrophages rest | 0.0 | Lung | 35.8 |
| Macrophages LPS | 0.0 | Thymus | 45.4 |
| HUVEC none | 0.0 | Kidney | 55.1 |
| HUVEC starved | 0.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3407 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3407 Highest expression of the CG59241-01 gene is seen in fetal brain (CT=31.3). Furthermore, low to moderate levels of expression is also observed in CNS cancer cell lines (CTs=32-34). The CG59241-01 gene codes for a putative amiloride-sensitive sodium channel. A similar amiloride-sensitive sodium channel was shown to be highly expressed in malignant glioblastoma multiforme tumors and to be a characteristic feature of malignant brain tumor cells (Ref.1). Therefore, therapeutic modulation of the activity of the protein encoded by this gene may be beneficial in the treatment of CNS cancer. Significant expression is also seen in a cluster of cell lines derived from brain, colon, breast, and ovarian cancers. Therefore, therapeutic modulation of the activity of this gene or its protein product, through the use of small molecule drugs, protein therapeutics or antibodies, might be beneficial in the treatment of these cancers.

cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system

disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

References:

1. Bubien JK, Keeton DA, Fuller CM, Gillespie GY, Reddy AT, Mapstone TB, Benos DJ. (1999) Malignant human gliomas express an amiloride-sensitive Na⁺ conductance. Am J Physiol 276(6 Pt 1):C1405-10

Panel 4D Summary: Ag3407 Highest expression Of the CG59241-01 gene is detected in PWM treated B lymphocytes (CT=32). Similar expression is also detected in primary activated Th1, Th2 and Tr1 cells, as well as TNF alpha treated dermal fibroblast CCD1070 cells (CTs=32). Therefore, expression of this gene can be used to distinguish these samples from other samples in the panel. Furthermore, this gene is expressed in activated lymphocytes. Likewise, no expression of this gene is seen in PBMC that contain normal B cells (CT=40), but it is induced when PBMC are treated with the pokeweed mitogen or PHA-L (CTs=34). In addition, the transcript is not seen in the B cell lymphoma Ramos regardless of stimulation. Therefore, the gene product could potentially be used therapeutically in the treatment of Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, psoriasis and in other diseases in which T cells and B cells are activated.

In addition, low expression of this gene is also observed in normal colon, lung, thymus and kidney tissues. The CG59241-01 gene encodes an amiloride-sensitive sodium channel. A similar channel, the amiloride-sensitive epithelial sodium channel (ENaC) constitutes the limiting step for sodium reabsorption in epithelial cells that line the distal nephron, distal colon, ducts of several exocrine glands and lung airways and plays an important role in pathophysiological and clinical conditions such as hypertension or lung edema. ENaC has been implicated in two genetic diseases, Liddle's syndrome and pseudohypoaldosteronism (PHA-1) (Ref.1). Therefore, antibody or small molecule therapies designed with the protein encoded for by CG59241-01 gene could modulate kidney/colon/lung function and be important in the treatment of inflammatory or autoimmune diseases of these tissues in addition

Reference:

1. Hummler E. (1998) Reversal of convention: from man to experimental animal in elucidating the function of the renal amiloride-sensitive sodium channel. *Exp Nephrol* 1998 Jul-Aug;6(4):265-71

AH. CG58602-01: FAD binding domain containing protein

Expression of gene CG58602-01 was assessed using the primer-probe set Ag3385, described in Table AHA. Results of the RTQ-PCR runs are shown in Tables AHB, AHC and AHD.

Table AHA. Probe Name Ag3385

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-tcatgaatccaggcaaagtg-3' | 20 | 1427 | 499 |
| Probe | TET-5'-ttagcccacaagttccctgactacgg-3' - TAMRA | 26 | 1468 | 500 |
| Reverse | 5'-tggcatgaagaaaagttcca-3' | 20 | 1503 | 501 |

Table AHB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3385, Run 210154892 | Tissue Name | Rel. Exp.(%) Ag3385, Run 210154892 |
|---------------------------|---------------------------------------|----------------------------------|---------------------------------------|
| AD 1 Hippo | 34.6 | Control (Path) 3 Temporal Ctx | 21.2 |
| AD 2 Hippo | 47.6 | Control (Path) 4 Temporal Ctx | 36.1 |
| AD 3 Hippo | 11.9 | AD 1 Occipital Ctx | 28.1 |
| AD 4 Hippo | 24.3 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 Hippo | 56.3 | AD 3 Occipital Ctx | 15.0 |
| AD 6 Hippo | 63.3 | AD 4 Occipital Ctx | 34.9 |
| Control 2 Hippo | 42.6 | AD 5 Occipital Ctx | 52.1 |
| Control 4 Hippo | 24.7 | AD 6 Occipital Ctx | 25.3 |
| Control (Path) 3 Hippo | 23.3 | Control 1 Occipital Ctx | 14.3 |
| AD 1 Temporal Ctx | 23.8 | Control 2 Occipital Ctx | 69.3 |
| | | Control 3 Occipital | |

| Sample | RTQ-PCR | RTA |
|-------------------|---------|------------------|
| AD 4 Temporal Ctx | 39.0 | Control (Path) 1 |

| | | | |
|----------------------------------|-------|-----------------------------------|------|
| | | Occipital Ctx | |
| AD 5 Inf Temporal Ctx | 100.0 | Control (Path) 2 Occipital Ctx | 11.0 |
| AD 5 Sup Temporal Ctx | 55.5 | Control (Path) 3 Occipital Ctx | 8.9 |
| AD 6 Inf Temporal Ctx | 64.2 | Control (Path) 4 Occipital Ctx | 17.3 |
| AD 6 Sup Temporal Ctx | 54.0 | Control 1 Parietal Ctx | 32.8 |
| Control 1 Temporal Ctx | 23.8 | Control 2 Parietal Ctx | 62.0 |
| Control 2 Temporal Ctx | 50.3 | Control 3 Parietal Ctx | 33.4 |
| Control 3 Temporal Ctx | 38.4 | Control (Path) 1 Parietal Ctx | 70.7 |
| Control 3 Temporal Ctx | 19.2 | Control (Path) 2 Parietal Ctx | 31.4 |
| Control (Path) 1 Temporal Ctx | 56.6 | Control (Path) 3 Parietal Ctx | 20.9 |
| Control (Path) 2 Temporal Ctx | 47.6 | Control (Path) 4 Parietal Ctx | 43.2 |

Table AHC. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3385, Run 217043538 | Tissue Name | Rel. Exp.(%) Ag3385, Run 217043538 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 2.4 | Renal ca. TK-10 | 3.5 |
| Melanoma* Hs688(A).T | 0.7 | Bladder | 6.6 |
| Melanoma* Hs688(B).T | 1.1 | Gastric ca. (liver met.) NCI-N87 | 2.1 |
| Melanoma* M14 | 0.9 | Gastric ca. KATO III | 0.9 |
| Melanoma* LOXIMVI | 1.3 | Colon ca. SW-948 | 4.5 |
| Melanoma* SK-MEL-5 | 2.2 | Colon ca. SW480 | 0.8 |
| Squamous cell carcinoma SCC-4 | 0.1 | Colon ca.* (SW480 met) SW620 | 1.3 |
| Testis Pool | 1.3 | Colon ca. HT29 | 0.6 |
| Prostate ca.* (bone met) PC-3 | 5.8 | Colon ca. HCT-116 | 1.9 |

| | | | |
|-------------|-----|--------------------|-----|
| Uterus Pool | 0.5 | Colon ca. SW1116 | 0.9 |
| Ovarian ca. | 1.1 | Colon ca. Colo-205 | 3.5 |

| | | | |
|-----------------------|-------|-------------------------------------|------|
| OVCAR-3 | | | |
| Ovarian ca. SK-OV-3 | 3.7 | Colon ca. SW-48 | 4.2 |
| Ovarian ca. OVCAR-4 | 0.2 | Colon Pool | 3.0 |
| Ovarian ca. OVCAR-5 | 42.0 | Small Intestine Pool | 3.5 |
| Ovarian ca. IGROV-1 | 8.0 | Stomach Pool | 1.8 |
| Ovarian ca. OVCAR-8 | 2.7 | Bone Marrow Pool | 0.9 |
| Ovary | 3.3 | Fetal Heart | 12.9 |
| Breast ca. MCF-7 | 10.3 | Heart Pool | 8.3 |
| Breast ca. MDA-MB-231 | 3.0 | Lymph Node Pool | 3.5 |
| Breast ca. BT 549 | 1.3 | Fetal Skeletal Muscle | 2.6 |
| Breast ca. T47D | 100.0 | Skeletal Muscle Pool | 25.5 |
| Breast ca. MDA-N | 0.4 | Spleen Pool | 0.2 |
| Breast Pool | 3.1 | Thymus Pool | 2.7 |
| Trachea | 3.2 | CNS cancer (glio/astro) U87-MG | 4.0 |
| Lung | 2.9 | CNS cancer (glio/astro) U-118-MG | 1.3 |
| Fetal Lung | 3.0 | CNS cancer (neuro;met) SK-N-AS | 1.8 |
| Lung ca. NCI-N417 | 0.2 | CNS cancer (astro) SF-539 | 1.3 |
| Lung ca. LX-1 | 1.1 | CNS cancer (astro) SNB-75 | 0.9 |
| Lung ca. NCI-H146 | 0.4 | CNS cancer (glio) SNB-19 | 5.0 |
| Lung ca. SHP-77 | 3.1 | CNS cancer (glio) SF-295 | 5.5 |
| Lung ca. A549 | 4.3 | Brain (Amygdala) Pool | 5.5 |
| Lung ca. NCI-H526 | 0.4 | Brain (cerebellum) | 13.5 |
| Lung ca. NCI-H23 | 6.8 | Brain (fetal) | 5.6 |
| Lung ca. NCI-H460 | 1.5 | Brain (Hippocampus) Pool | 5.2 |
| Lung ca. HOP-62 | 0.1 | Cerebral Cortex Pool | 7.1 |
| Lung ca. NCI-H522 | 3.6 | Brain (Substantia nigra) | 11.5 |

| | | | |
|-----------------|-----|------------------|-----|
| Metastatic | | Brain (WHOIC) | |
| Liver ca. HepG2 | 2.7 | Spinal Cord Pool | 4.8 |

| | | | |
|-----------------|-----|-----------------------|-----|
| Kidney Pool | 6.2 | Adrenal Gland | 6.0 |
| Fetal Kidney | 4.0 | Pituitary gland Pool | 1.7 |
| Renal ca. 786-0 | 0.2 | Salivary Gland | 6.6 |
| Renal ca. A498 | 1.4 | Thyroid (female) | 5.2 |
| Renal ca. ACHN | 0.8 | Pancreatic ca. CAPAN2 | 3.5 |
| Renal ca. UO-31 | 0.9 | Pancreas Pool | 4.4 |

Table AHD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3385, Run 165296471 | Tissue Name | Rel. Exp.(%) Ag3385, Run 165296471 |
|-------------------------------|--|---|--|
| Secondary Th1 act | 1.2 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 3.6 | HUVEC IFN gamma | 3.7 |
| Secondary Tr1 act | 2.6 | HUVEC TNF alpha + IFN gamma | 0.7 |
| Secondary Th1 rest | 0.4 | HUVEC TNF alpha + IL4 | 2.2 |
| Secondary Th2 rest | 0.9 | HUVEC IL-11 | 1.3 |
| Secondary Tr1 rest | 0.4 | Lung Microvascular EC none | 3.2 |
| Primary Th1 act | 1.1 | Lung Microvascular EC TNFalpha + IL-1beta | 1.5 |
| Primary Th2 act | 0.7 | Microvascular Dermal EC none | 3.0 |
| Primary Tr1 act | 0.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 1.1 | Bronchial epithelium TNFalpha + IL1beta | 0.6 |
| Primary Th2 rest | 0.5 | Small airway epithelium none | 0.7 |
| Primary Tr1 rest | 0.6 | Small airway epithelium TNFalpha + IL-1beta | 0.8 |
| CD45RA CD4 lymphocyte act | 2.0 | Coronery artery SMC rest | 0.5 |
| CD45RO CD4 lymphocyte act | 3.7 | Coronery artery SMC TNFalpha + IL-1beta | 2.0 |
| CD8 lymphocyte act | 0.9 | Astrocytes rest | 1.5 |
| Secondary CD8 lymphocyte rest | 2.7 | Astrocytes TNFalpha + IL-1beta | 2.6 |
| Secondary CD8 | 0.0 | KT-812 (Basophil) rest | 3.0 |

| | | |
|---------------------------|-----|-------------------------------|
| Primary Th1 Th2 Tr1 anti- | 0.0 | MA 700HIVC |
| | | [CCD1106 (Keratinocytes)] 3.3 |

| | | | |
|---------------------------------|------|--|--------------|
| CD95 CH11 | | none | |
| LAK cells rest | 9.4 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.3 |
| LAK cells IL-2 | 0.8 | Liver cirrhosis | 7.9 |
| LAK cells IL-2+IL-12 | 1.5 | Lupus kidney | 2.3 |
| LAK cells IL-2+IFN gamma | 3.7 | NCI-H292 none | 3.3 |
| LAK cells IL-2+ IL-18 | 2.5 | NCI-H292 IL-4 | 8.4 |
| LAK cells PMA/ionomycin | 2.0 | NCI-H292 IL-9 | 2.6 |
| NK Cells IL-2 rest | 0.7 | NCI-H292 IL-13 | 2.9 |
| Two Way MLR 3 day | 4.6 | NCI-H292 IFN gamma | 1.8 |
| Two Way MLR 5 day | 2.8 | HPAEC none | 2.3 |
| Two Way MLR 7 day | 1.8 | HPAEC TNF alpha + IL-1 beta | 1.9 |
| PBMC rest | 0.6 | Lung fibroblast none | 1.5 |
| PBMC PWM | 11.0 | Lung fibroblast TNF alpha + IL-1 beta | 0.7 |
| PBMC PHA-L | 2.3 | Lung fibroblast IL-4 | 1.6 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 2.0 |
| Ramos (B cell) ionomycin | 0.9 | Lung fibroblast IL-13 | 0.9 |
| B lymphocytes PWM | 3.5 | Lung fibroblast IFN gamma | 0.7 |
| B lymphocytes CD40L and IL-4 | 5.4 | Dermal fibroblast CCD1070 rest | 1.6 |
| EOL-1 dbcAMP | 5.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 |
| EOL-1 dbcAMP PMA/ionomycin | 1.2 | Dermal fibroblast CCD1070 IL-1 beta | 2.3 |
| Dendritic cells none | 15.5 | Dermal fibroblast IFN gamma | 0.5 |
| Dendritic cells LPS | 4.5 | Dermal fibroblast IL-4 | 0.4 |
| Dendritic cells anti- CD40 | 11.7 | IBD Colitis 2 | 0.3 |
| Monocytes rest | 8.7 | IBD Crohn's | 0.0 |
| Monocytes LPS | 0.6 | Colon | 5.1 |
| Macrophages rest | 13.5 | Lung | 6.7 |
| Macrophages LPS | 1.6 | Thymus | 100.0 |
| HUVEC none | 0.6 | Kidney | 11.3 |

CNS_neurodegeneration_v1.0_Summary.xls (857) This panel contains the expression of CG58602-01 gene at low levels in the brains of an independent group of individuals.

However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3385 Highest expression of the CG58602-01 gene is seen in a breast cancer cell line (CT=26.3). Significant expression is also seen in an ovarian cancer cell line. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of breast and ovarian cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of breast and ovarian cancers.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that deregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

Expression of this gene is higher in fetal skeletal muscle (CT=28.3) when compared to expression in adult skeletal muscle (CT=31.5). Thus, expression of this gene could be used to distinguish fetal from adult skeletal muscle.

In addition, this gene is expressed at high levels (CTs=29-30.4) in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3385 Highest expression of the CG58602-01 gene is seen in the thymus (CT=28). Thus, the putative protein encoded for by this gene could therefore play an important role in T cell development. Therefore, small molecule therapeutics designed against

AI. CG58468-01: Serum Amyloid P Component

Expression of gene CG58468-01 was assessed using the primer-probe set Ag3356, described in Table AIA. Results of the RTQ-PCR runs are shown in Table AIB.

Table AIA. Probe Name Ag3356

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -aggcatttattttccctcaaga-3' | 22 | 106 | 502 |
| Probe | TET-5'-agtctatgtgtccctgatccccagg-3' TAMRA | 26 | 137 | 503 |
| Reverse | 5'-gtttcaggcaaagttgaagt-3' | 22 | 181 | 504 |

Table AIB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3356, Run 216523476 | Tissue Name | Rel. Exp.(%) Ag3356, Run 216523476 |
|-------------------------------|------------------------------------|----------------------------------|------------------------------------|
| Adipose | 2.2 | Renal ca. TK-10 | 0.0 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 0.0 |
| Melanoma* Hs688(B).T | 0.0 | Gastric ca. (liver met.) NCI-N87 | 0.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 0.0 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |
| Melanoma* SK-MEL-5 | 0.0 | Colon ca. SW480 | 0.0 |
| Squamous cell carcinoma SCC-4 | 0.0 | Colon ca.* (SW480 met) SW620 | 0.0 |
| Testis Pool | 1.7 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 0.0 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 0.0 |
| Placenta | 0.0 | Colon cancer tissue | 0.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.0 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.0 | Colon ca. SW-48 | 0.0 |

| | | | |
|-----------------------|-----|----------------------|-----|
| Ovarian ca OVCAR-5 | 0.0 | Small Intestine Pool | 2.0 |
|-----------------------|-----|----------------------|-----|

| | | | |
|-----------------------|------|--------------------------------------|------|
| Ovarian ca. IGROV-1 | 0.0 | Stomach Pool | 0.0 |
| Ovarian ca. OVCAR-8 | 0.0 | Bone Marrow Pool | 10.7 |
| Ovary | 0.0 | Fetal Heart | 0.0 |
| Breast ca. MCF-7 | 0.0 | Heart Pool | 2.6 |
| Breast ca. MDA-MB-231 | 0.0 | Lymph Node Pool | 25.9 |
| Breast ca. BT 549 | 0.0 | Fetal Skeletal Muscle | 2.1 |
| Breast ca. T47D | 0.0 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 0.0 |
| Breast Pool | 19.6 | Thymus Pool | 0.0 |
| Trachea | 1.5 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 0.0 | CNS cancer (glio/astro) UJ-118-MG | 0.0 |
| Fetal Lung | 5.0 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 0.0 | CNS cancer (astro) SNB-75 | 0.0 |
| Lung ca. NCI-H146 | 0.0 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 0.0 | CNS cancer (glio) SF-295 | 0.0 |
| Lung ca. A549 | 0.0 | Brain (Amygdala) Pool | 0.0 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 0.0 |
| Lung ca. NCI-H23 | 38.7 | Brain (fetal) | 2.6 |
| Lung ca. NCI-H460 | 0.0 | Brain (Hippocampus) Pool | 0.0 |
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 0.0 |
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) Pool | 0.0 |
| Liver | 2.3 | Brain (Thalamus) Pool | 0.0 |
| Fetal Liver | 0.0 | Brain (whole) | 0.0 |
| Liver ca. HepG2 | 0.0 | Spinal Cord Pool | 2.1 |
| Kidney Pool | 19.1 | Adrenal Gland | 0.0 |
| Fetal Kidney | 0.0 | Pituitary gland Pool | 2.1 |
| Renal ca. 786-O | 0.0 | Salivary Gland | 0.0 |

| | | |
|-----------------|-----|---------------|
| Renal ca. UO-31 | 0.0 | Pancreas Pool |
|-----------------|-----|---------------|

CNS_neurodegeneration_v1.0 Summary: Ag3356 Expression of the CG58468-01 gene is low/undetectable in all the samples on this panel. (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3356 Expression of the CG58468-01 gene is restricted to the colon (CT=34). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel.

Panel 4D Summary: Ag3356 Results from one experiment with the CG56003-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

AJ. CG58183-01: N-METHYL-D-ASPARTATE RECEPTOR

Expression of gene CG58183-01 was assessed using the primer-probe set Ag3355, described in Table AJA. Results of the RTQ-PCR runs are shown in Tables AJB, AJC and AJD.

Table AJA. Probe Name Ag3355

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -gctggccaactctgtctagac -3' | 21 | 1617 | 505 |
| Probe | TET-5' -tgactcttccacattggacagccttt -3' - TAMRA | 26 | 1649 | 506 |
| Reverse | 5' -ttactgcatggaggctgtaa -3' | 22 | 1675 | 507 |

Table AJB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3355, Run 210142850 | Tissue Name | Rel. Exp.(%) Ag3355, Run 210142850 |
|-------------|---------------------------------------|----------------------------------|---------------------------------------|
| AD 1 Hippo | 17.7 | Control (Path) 3 Temporal Ctx | 7.3 |
| AD 2 Hippo | 27.4 | Control (Path) 4 Temporal Ctx | 47.6 |
| AD 3 Hippo | 8.8 | AD 1 Occipital Ctx | 18.8 |
| AD 4 Hippo | 16.2 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 Hippo | 53.6 | AD 3 Occipital Ctx | 3.0 |
| AD 6 Hippo | 51.4 | AD 4 Occipital Ctx | 27.2 |

| Sample | Rel. Exp.(%) | Sample | Rel. Exp.(%) |
|-------------------------|--------------|----------------------------|--------------|
| Control (Path) Hippo | 4.5 | Control 1 Occipital Ctx | 2.8 |

| | | | |
|-------------------------------|------|--------------------------------|-------|
| AD 1 Temporal Ctx | 18.3 | Control 2 Occipital Ctx | 39.0 |
| AD 2 Temporal Ctx | 48.0 | Control 3 Occipital Ctx | 18.2 |
| AD 3 Temporal Ctx | 5.7 | Control 4 Occipital Ctx | 3.4 |
| AD 4 Temporal Ctx | 15.2 | Control (Path) 1 Occipital Ctx | 81.8 |
| AD 5 Inf Temporal Ctx | 61.6 | Control (Path) 2 Occipital Ctx | 9.0 |
| AD 5 Sup Temporal Ctx | 69.3 | Control (Path) 3 Occipital Ctx | 0.0 |
| AD 6 Inf Temporal Ctx | 66.9 | Control (Path) 4 Occipital Ctx | 13.3 |
| AD 6 Sup Temporal Ctx | 62.9 | Control 1 Parietal Ctx | 6.6 |
| Control 1 Temporal Ctx | 8.5 | Control 2 Parietal Ctx | 74.7 |
| Control 2 Temporal Ctx | 66.9 | Control 3 Parietal Ctx | 21.0 |
| Control 3 Temporal Ctx | 34.9 | Control (Path) 1 Parietal Ctx | 100.0 |
| Control 3 Temporal Ctx | 7.0 | Control (Path) 2 Parietal Ctx | 21.9 |
| Control (Path) 1 Temporal Ctx | 90.1 | Control (Path) 3 Parietal Ctx | 6.0 |
| Control (Path) 2 Temporal Ctx | 74.7 | Control (Path) 4 Parietal Ctx | 50.7 |

Table AJC_General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3355, Run 216523475 | Tissue Name | Rel. Exp.(%) Ag3355, Run 216523475 |
|----------------------|------------------------------------|----------------------------------|------------------------------------|
| Adipose | 0.0 | Renal ca. TK-10 | 0.0 |
| Melanoma* Hs688(A).T | 0.9 | Bladder | 0.0 |
| Melanoma* Hs688(B).T | 0.0 | Gastric ca. (liver met.) NCI-N87 | 0.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 0.0 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |

Squamous cell carcinoma SCC-4

0.0

Oto ca * (SW48)
met) SW620

0.0

| | | | |
|-------------------------------|------|-------------------------------------|------|
| Testis Pool | 2.4 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 0.0 |
| Prostate Pool | 2.1 | Colon ca. CaCo-2 | 0.0 |
| Placenta | 0.0 | Colon cancer tissue | 0.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.4 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.3 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.0 | Colon Pool | 2.2 |
| Ovarian ca. OVCAR-5 | 0.0 | Small Intestine Pool | 3.4 |
| Ovarian ca. IGROV-1 | 0.0 | Stomach Pool | 2.4 |
| Ovarian ca. OVCAR-8 | 0.0 | Bone Marrow Pool | 1.5 |
| Ovary | 4.4 | Fetal Heart | 1.9 |
| Breast ca. MCF-7 | 0.0 | Heart Pool | 3.6 |
| Breast ca. MDA-MB-231 | 0.0 | Lymph Node Pool | 2.9 |
| Breast ca. BT 549 | 0.0 | Fetal Skeletal Muscle | 1.8 |
| Breast ca. T47D | 0.0 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 4.3 |
| Breast Pool | 5.7 | Thymus Pool | 4.7 |
| Trachea | 1.7 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 1.6 | CNS cancer (glio/astro) U-118-MG | 0.1 |
| Fetal Lung | 0.0 | CNS cancer (neuro;met) SK-N-AS | 3.2 |
| Lung ca. NCI-N417 | 17.8 | CNS cancer (astro) SF-539 | 14.8 |
| Lung ca. LX-1 | 0.0 | CNS cancer (astro) SNB-75 | 17.6 |
| Lung ca. NCI-H146 | 4.0 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 11.7 | CNS cancer (glio) SF-295 | 0.0 |

| | | | |
|-------------------|-----|---------------------|--------|
| Lung ca. NCI-H12 | | Brain (Cerebellum) | 0.00,0 |
| Lung ca. NCI-H460 | 0.3 | Brain (Hippocampus) | 33.0 |

| | | Pool | |
|-------------------|-----|-------------------------------|------|
| Lung ca. HOP-62 | 0.3 | Cerebral Cortex Pool | 42.3 |
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) Pool | 43.8 |
| Liver | 0.2 | Brain (Thalamus) Pool | 50.7 |
| Fetal Liver | 0.4 | Brain (whole) | 71.2 |
| Liver ca. HepG2 | 0.0 | Spinal Cord Pool | 15.0 |
| Kidney Pool | 1.4 | Adrenal Gland | 0.0 |
| Fetal Kidney | 7.2 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 0.1 |
| Renal ca. A498 | 0.0 | Thyroid (female) | 0.1 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 0.0 |
| Renal ca. UO-31 | 0.0 | Pancreas Pool | 2.7 |

Table AJD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3355, Run 165241988 | Tissue Name | Rel. Exp.(%) Ag3355, Run 165241988 |
|---------------------------|--|---|--|
| Secondary Th1 act | 0.0 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 0.0 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 0.0 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 11.8 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 0.0 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 0.0 |
| Primary Tr1 act | 0.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 0.0 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 0.0 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | | IFNalpha + IL-1beta | |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 0.0 |

| | | | |
|---------------------------|-----|---------------------|-----|
| CD45RA CD4 lymphocyte act | | IFNalpha + IL-1beta | |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 0.0 |

| | | | |
|--------------------------------|-----|---|------|
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 57.8 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 67.4 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 0.0 |
| LAK cells rest | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 39.8 |
| LAK cells IL-2+IL-12 | 0.0 | Lupus kidney | 0.0 |
| LAK cells IL-2+IFN gamma | 0.0 | NCI-H292 none | 0.0 |
| LAK cells IL-2+ IL-18 | 0.0 | NCI-H292 IL-4 | 0.0 |
| LAK cells PMA/ionomycin | 0.0 | NCI-H292 IL-9 | 0.0 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 0.0 |
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 0.0 |
| Two Way MLR 5 day | 0.0 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 0.0 |
| PBMC PWM | 0.0 | Lung fibroblast TNF alpha + IL-1 beta | 0.0 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 0.0 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 0.0 |
| B lymphocytes PWM | 0.0 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 rest | 0.0 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 0.0 | Dermal fibroblast IL-4 | 0.0 |

| MONOCYTES TEST | | DERMAL FIBROBLAST | |
|----------------|-----|-------------------|------|
| Monocytes LPS | 0.0 | Colon | 12.7 |

| | | | |
|------------------|-----|--------|-------|
| Macrophages rest | 0.0 | Lung | 15.2 |
| Macrophages LPS | 0.0 | Thymus | 100.0 |
| HUVEC none | 0.0 | Kidney | 73.2 |
| HUVEC starved | 0.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3355 This panel confirms the expression of CG58183-01 gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3355 Highest expression of CG58183-01 gene is detected in fetal brain ($C_t=29.2$). In addition, this gene is expressed at high levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord ($CTs= 29-32$). Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene codes for N-methyl-D-aspartate (NMDA) receptor 3A protein. In cats and rodent models competitive NMDA receptor antagonists, such as D-(E)-4-(3-phosphonoprop-2-enyl)piperazine-2-carboxylic acid, which act at the neurotransmitter recognition site were shown to be effective in reducing ischaemic brain damage when administered prior to the onset of an ischaemic episode (Ref. 1). Therefore, therapeutic modulation of the activity of the protein encoded by this gene may be beneficial in the treatment of ischaemic brain.

Among tissues with metabolic or endocrine function, this gene is expressed at low levels in pancreas, heart, and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

Furthermore, low to moderate expression of this gene is detected in lung cancer, and CNS cancer cell lines. Therefore, therapeutic modulation of the activity of this gene or its

References:

1. McCulloch J. (1991) Ischaemic brain damage--prevention with competitive and non-competitive antagonists of N-methyl-D-aspartate receptors. *Arzneimittelforschung* 41(3A):319-24.

Panel 4D Summary: Ag3355 Expression of the CG58183-01 gene is limited to a few samples, with highest expression in the thymus (CT=33.5). Thus, expression of this gene may be useful as a marker of thymic tissue. Low, but significant levels of expression are also seen in the kidney, in TNF-alpha and IL-1 beta treated astrocytes and in the PMA/ionomycin treated basophil cell line KU-812. Thus, this gene product may be involved in the normal homeostasis of this tissue. Therefore, agonistic antibodies or protein therapeutics may be important in the treatment of inflammatory or autoimmune diseases that affect the kidney, including lupus and glomerulonephritis. In addition, the expression of this transcript in astrocytes treated with TNF-a and IL-1 indicates that therapeutics designed against the protein encoded by this gene may be useful for the treatment of inflammatory CNS diseases such as multiple sclerosis.

AK. CG59315-01: connexin

Expression of gene CG59315-01 was assessed using the primer-probe set Ag3542, described in Table AKA. Results of the RTQ-PCR runs are shown in Tables AKB and AKC.

Table AKA. Probe Name Ag3542

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -ggacacccctccaaccttagatc-3' | 21 | 1024 | 508 |
| Probe | TET-5'-tacctgtttccttcattgaggctgg-3' TAMRA | 26 | 1046 | 509 |
| Reverse | 5' -ttgcattttgtgtccatgag-3' | 21 | 1081 | 510 |

Table AKB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3542, Run 217049297 | Tissue Name | Rel. Exp.(%) Ag3542, Run 217049297 |
|-------------|---------------------------------------|-----------------|---------------------------------------|
| Adipose | 17.3 | Renal ca. TK-10 | 6.8 |
| Melanoma* | | | |

| Hs058(B), 1 | NCF-N8 |
|---------------|----------------------|
| Melanoma* M14 | Gastric ca. KATO III |

| | | | |
|-------------------------------|-------|-------------------------------------|------|
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 3.8 |
| Melanoma* SK-MEL-5 | 0.7 | Colon ca. SW480 | 39.0 |
| Squamous cell carcinoma SCC-4 | 2.0 | Colon ca.* (SW480 met) SW620 | 6.7 |
| Testis Pool | 0.3 | Colon ca. HT29 | 2.3 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 17.7 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 2.8 |
| Placenta | 1.2 | Colon cancer tissue | 1.6 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.3 |
| Ovarian ca. OVCAR-3 | 6.3 | Colon ca. Colo-205 | 0.3 |
| Ovarian ca. SK-OV-3 | 2.5 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.0 | Colon Pool | 1.7 |
| Ovarian ca. OVCAR-5 | 25.0 | Small Intestine Pool | 6.3 |
| Ovarian ca. IGROV-1 | 6.4 | Stomach Pool | 5.4 |
| Ovarian ca. OVCAR-8 | 0.0 | Bone Marrow Pool | 3.1 |
| Ovary | 0.6 | Fetal Heart | 1.7 |
| Breast ca. MCF-7 | 12.9 | Heart Pool | 1.5 |
| Breast ca. MDA-MB-231 | 5.0 | Lymph Node Pool | 3.6 |
| Breast ca. BT 549 | 8.7 | Fetal Skeletal Muscle | 0.0 |
| Breast ca. T47D | 100.0 | Skeletal Muscle Pool | 6.1 |
| Breast ca. MDA-N | 2.7 | Spleen Pool | 5.8 |
| Breast Pool | 4.9 | Thymus Pool | 3.0 |
| Trachea | 9.3 | CNS cancer (glio/astro) U87-MG | 1.0 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 13.7 |
| Fetal Lung | 3.2 | CNS cancer (neuro;met) SK-N-AS | 35.4 |
| Lung ca. NCI-N417 | 1.2 | CNS cancer (astro) SF-539 | 4.9 |

Lung ca. NCI-H446

CNS cancer (astro)

SNB-19

Lung ca. SHP-77

8.1

CNS cancer (glio) SF-

12.5

| | | 295 | |
|-------------------|------|-------------------------------|------|
| Lung ca. A549 | 10.8 | Brain (Amygdala) Pool | 0.4 |
| Lung ca. NCI-H526 | 2.1 | Brain (cerebellum) | 13.6 |
| Lung ca. NCI-H23 | 8.1 | Brain (fetal) | 6.9 |
| Lung ca. NCI-H460 | 0.8 | Brain (Hippocampus) Pool | 1.5 |
| Lung ca. HOP-62 | 10.2 | Cerebral Cortex Pool | 0.0 |
| Lung ca. NCI-H522 | 4.9 | Brain (Substantia nigra) Pool | 0.2 |
| Liver | 0.0 | Brain (Thalamus) Pool | 1.2 |
| Fetal Liver | 1.2 | Brain (whole) | 0.0 |
| Liver ca. HepG2 | 0.0 | Spinal Cord Pool | 0.4 |
| Kidney Pool | 3.1 | Adrenal Gland | 2.0 |
| Fetal Kidney | 0.0 | Pituitary gland Pool | 1.8 |
| Renal ca. 786-0 | 6.3 | Salivary Gland | 3.2 |
| Renal ca. A498 | 0.0 | Thyroid (female) | 3.8 |
| Renal ca. ACHN | 12.1 | Pancreatic ca. CAPAN2 | 0.0 |
| Renal ca. UO-31 | 3.2 | Pancreas Pool | 4.2 |

Table AKC. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3542, Run 166453844 | Tissue Name | Rel. Exp.(%) Ag3542, Run 166453844 |
|--------------------|---|---|---|
| Secondary Th1 act | 3.9 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 5.4 | HUVEC IFN gamma | 2.4 |
| Secondary Tr1 act | 3.8 | HUVEC TNF alpha + IFN gamma | 0.4 |
| Secondary Th1 rest | 33.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 5.3 | HUVEC IL-11 | 1.4 |
| Secondary Tr1 rest | 14.8 | Lung Microvascular EC none | 3.1 |
| Primary Th1 act | 6.1 | Lung Microvascular EC TNFalpha + IL-1beta | 1.9 |
| Primary Th2 act | 0.6 | Microvascular Dermal EC none | 1.9 |
| Primary Tr1 act | 5.5 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 84.7 | Bronchial epithelium TNFalpha + IL-1beta | 2.7 |
| Primary Tr1 rest | 16.0 | Small airway epithelium TNFalpha + IL-1beta | 3.8 |

| | | | |
|--------------------------------|------|---|------|
| CD45RA CD4 lymphocyte act | 0.3 | Coronery artery SMC rest | 2.1 |
| CD45RO CD4 lymphocyte act | 3.6 | Coronery artery SMC TNFalpha + IL-1beta | 0.5 |
| CD8 lymphocyte act | 0.9 | Astrocytes rest | 5.8 |
| Secondary CD8 lymphocyte rest | 2.5 | Astrocytes TNFalpha + IL-1beta | 12.0 |
| Secondary CD8 lymphocyte act | 12.6 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 13.6 | KU-812 (Basophil) PMA/ionomycin | 5.4 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 40.6 | CCD1106 (Keratinocytes) none | 1.7 |
| LAK cells rest | 3.7 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 4.9 |
| LAK cells IL-2 | 7.6 | Liver cirrhosis | 81.2 |
| LAK cells IL-2+IL-12 | 7.9 | Lupus kidney | 5.0 |
| LAK cells IL-2+IFN gamma | 11.7 | NCI-H292 none | 7.8 |
| LAK cells IL-2+ IL-18 | 7.2 | NCI-H292 IL-4 | 3.5 |
| LAK cells PMA/ionomycin | 3.8 | NCI-H292 IL-9 | 6.0 |
| NK Cells IL-2 rest | 8.0 | NCI-H292 IL-13 | 6.4 |
| Two Way MLR 3 day | 2.3 | NCI-H292 IFN gamma | 2.4 |
| Two Way MLR 5 day | 0.9 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.9 |
| PBMC rest | 12.8 | Lung fibroblast none | 0.0 |
| PBMC PWM | 5.4 | Lung fibroblast TNF alpha + IL-1 beta | 1.1 |
| PBMC PHA-L | 3.7 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 1.9 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 0.4 |
| B lymphocytes PWM | 3.7 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 4.4 | Dermal fibroblast CCD1070 rest | 0.4 |
| EOL-1 dbcAMP | 14.1 | Dermal fibroblast CCD1070 TNF alpha | 18.0 |

Dermal fibroblast

Dermal fibroblast

Dendritic cells none

Dendritic cells none

Dendritic cells LPS

1.4

Dermal fibroblast IL-4

1.4

| | | | |
|---------------------------|------|---------------|-------|
| Dendritic cells anti-CD40 | 2.3 | IBD Colitis 2 | 4.0 |
| Monocytes rest | 53.2 | IBD Crohn's | 3.2 |
| Monocytes LPS | 19.2 | Colon | 100.0 |
| Macrophages rest | 0.6 | Lung | 11.1 |
| Macrophages LPS | 0.0 | Thymus | 2.7 |
| HUVEC none | 5.4 | Kidney | 7.7 |
| HUVEC starved | 4.3 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3542 Expression of the CG59315-01 gene is low/undetectable in all the samples on this panel. (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3542 Expression of the CG59315-01 gene is highest in a breast cancer cell line (CT=31.3). Furthermore, there is significant expression in a cluster of cell lines derived from brain cancer, colon cancer and ovarian cancer. Therefore, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of colon, brain, ovarian, and breast cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, brain, ovarian, and breast cancers.

Low but significant levels of expression are also seen in the cerebellum. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Among metabolic tissues, this gene is expressed at low levels in adipose. Therefore, this gene product may be useful in the treatment of obesity.

Panel 4D Summary: Ag3542 Expression of the CG59315-01 gene is highest in the normal colon (CT=30). Furthermore, expression is undetectable in colon samples from Crohn's and colitis patients. Thus, expression of this gene could be used to differentiate between normal and inflamed colon. This gene encodes a connexin homolog, a gap junction protein involved in intercellular communication.

therapeutic antibodies that block its function may also be useful in the treatment of a range of inflammatory and autoimmune diseases in which T cells and monocytes play a pivotal role.

These include, but are not limited to, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, or psoriasis.

References:

1. Kwak BR, Mulhaupt F, Veillard N, Gros DB, Mach F. Altered pattern of vascular connexin expression in atherosclerotic plaques. *Arterioscler Thromb Vasc Biol* 2002 Feb 1;22(2):225-30

AL. CG59203-01: Lysozyme C-like protein

Expression of gene CG59203-01 was assessed using the primer-probe set Ag3392, described in Table ALA. Results of the RTQ-PCR runs are shown in Tables ALB and ALC.

Table ALA. Probe Name Ag3392

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -tgtgagggtttctaaactggaa-3' | 22 | 540 | 511 |
| Probe | TET-5' -ctttgcagcaacgcctagggtt-3' - TAMRA | 24 | 576 | 512 |
| Reverse | 5' -tgacacaggcatttggacat-3' | 20 | 607 | 513 |

Table ALB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3392, Run 216821373 | Tissue Name | Rel. Exp.(%) Ag3392, Run 216821373 |
|-------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 0.0 | Renal ca. TK-10 | 2.7 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 0.0 |
| Melanoma* Hs688(B).T | 0.0 | Gastric ca. (liver met.) NCI-N87 | 0.7 |
| Melanoma* M14 | 1.2 | Gastric ca. KATO III | 0.4 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.6 |

| | | | |
|----------------------------------|-----|--------------------------------|-----|
| Squamous cell carcinoma SCC-4 | 0.0 | Renal ca. * SW48 met) SW620 | 0.0 |
|----------------------------------|-----|--------------------------------|-----|

| | | | |
|-------------------------------|--------------|-------------------------------------|------|
| Testis Pool | 100.0 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 0.0 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 1.2 |
| Placenta | 0.7 | Colon cancer tissue | 0.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.4 | Colon ca. Colo-205 | 11.6 |
| Ovarian ca. SK-OV-3 | 1.0 | Colon ca. SW-48 | 2.2 |
| Ovarian ca. OVCAR-4 | 0.0 | Colon Pool | 1.1 |
| Ovarian ca. OVCAR-5 | 0.0 | Small Intestine Pool | 0.4 |
| Ovarian ca. IGROV-1 | 0.0 | Stomach Pool | 0.0 |
| Ovarian ca. OVCAR-8 | 0.0 | Bone Marrow Pool | 1.3 |
| Ovary | 0.0 | Fetal Heart | 0.0 |
| Breast ca. MCF-7 | 15.2 | Heart Pool | 1.1 |
| Breast ca. MDA-MB-231 | 0.0 | Lymph Node Pool | 0.0 |
| Breast ca. BT 549 | 1.7 | Fetal Skeletal Muscle | 0.0 |
| Breast ca. T47D | 0.0 | Skeletal Muscle Pool | 0.5 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 0.0 |
| Breast Pool | 0.0 | Thymus Pool | 0.9 |
| Trachea | 1.1 | CNS cancer (glio/astro) U87-MG | 1.4 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.5 |
| Fetal Lung | 0.8 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 5.4 | CNS cancer (astro) SNB-75 | 6.1 |
| Lung ca. NCI-H146 | 0.0 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 0.0 | CNS cancer (glio) SF-295 | 0.0 |

| | | | |
|-------------------|-----|---------------------|-----|
| Lung ca. NCI-H128 | | Brain (cortex) | |
| Lung ca. NCI-H460 | 1.1 | Brain (Hippocampus) | 0.0 |

| | | Pool | |
|-------------------|------|-------------------------------|-----|
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 0.5 |
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) Pool | 0.0 |
| Liver | 1.5 | Brain (Thalamus) Pool | 0.9 |
| Fetal Liver | 1.2 | Brain (whole) | 0.0 |
| Liver ca. HepG2 | 18.3 | Spinal Cord Pool | 0.0 |
| Kidney Pool | 1.6 | Adrenal Gland | 0.0 |
| Fetal Kidney | 0.0 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 0.3 | Salivary Gland | 0.0 |
| Renal ca. A498 | 0.0 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 0.0 |
| Renal ca. UO-31 | 0.0 | Pancreas Pool | 0.0 |

Table ALC. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3392, Run 165296470 | Tissue Name | Rel. Exp.(%) Ag3392, Run 165296470 |
|--------------------|--|---|--|
| Secondary Th1 act | 0.0 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 36.9 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 0.0 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 0.0 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 0.0 |
| Primary Tr1 act | 0.0 | Microvascular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 0.0 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 0.0 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 | | | |

| | | | |
|--------------------|-----|---------------------|-----|
| CD4 lymphocyte act | 0.0 | CD4 lymphocyte rest | 0.0 |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 0.0 |

| | | | |
|--------------------------------|------|---|--------------|
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 0.0 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.0 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 0.0 |
| LAK cells rest | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 100.0 |
| LAK cells IL-2+IL-12 | 0.0 | Lupus kidney | 0.0 |
| LAK cells IL-2+IFN gamma | 0.0 | NCI-H292 none | 0.0 |
| LAK cells IL-2+ IL-18 | 0.0 | NCI-H292 IL-4 | 0.0 |
| LAK cells PMA/ionomycin | 16.8 | NCI-H292 IL-9 | 0.0 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 0.0 |
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 0.0 |
| Two Way MLR 5 day | 0.0 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 0.0 |
| PBMC PWM | 11.1 | Lung fibroblast TNF alpha + IL-1 beta | 0.0 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 0.0 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 0.0 |
| B lymphocytes PWM | 26.8 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 rest | 0.0 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 0.0 | Dermal fibroblast IL-4 | 0.0 |

| Monocytes LPS | 0.0 | Colon | 0.0 |
|---------------|-----|-------|-----|
| | | | |

| | | | |
|------------------|-----|--------|-----|
| Macrophages rest | 0.0 | Lung | 0.0 |
| Macrophages LPS | 0.0 | Thymus | 0.0 |
| HUVEC none | 0.0 | Kidney | 0.0 |
| HUVEC starved | 0.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3392 Expression of the CG59203-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3392 Highest expression of the CG59203-01 gene is seen in the testis. Thus, expression of this gene could be used as a marker of testicular tissue. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in treating infertility or hypogonadism.

Panel 4D Summary: Ag3392 Significant expression of this gene is detected in a liver cirrhosis sample (CT = 33.8). Furthermore, expression of this gene is not detected in normal liver in Panel 1.3D, suggesting that its expression is unique to liver cirrhosis. Therefore, therapeutic modulation of the expression or function of this gene may reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, expression of this gene could also be used for the diagnosis of liver cirrhosis.

AM. CG58662-01: cytoplasmic protein

Expression of gene CG58662-01 was assessed using the primer-probe set Ag3387, described in Table AMA. Results of the RTQ-PCR runs are shown in Tables AMB, AMC and AMD.

Table AMA. Probe Name Ag3387

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-aacctgcactccatgt-3' | 19 | 504 | 514 |
| Probe | TET-5'-agaccccgagggtatcctctgag-3'-TAMRA | 25 | 532 | 515 |
| Reverse | 5'-ctctgtcagtgcccacatct-3' | 20 | 564 | 516 |

Table AMB. CNS_neurodegeneration_v1.0

| Sample ID | AD 1 Hippo | Control (Path) | Temporal Ctx |
|-----------|------------|----------------|--------------|
| | 15.7 | | 7.3 |

| | | | |
|----------------------------------|-------|-----------------------------------|------|
| AD 2 Hippo | 34.6 | Control (Path) 4 Temporal Ctx | 42.0 |
| AD 3 Hippo | 5.5 | AD 1 Occipital Ctx | 17.9 |
| AD 4 Hippo | 9.7 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 Hippo | 95.3 | AD 3 Occipital Ctx | 5.4 |
| AD 6 Hippo | 33.9 | AD 4 Occipital Ctx | 19.6 |
| Control 2 Hippo | 41.5 | AD 5 Occipital Ctx | 61.1 |
| Control 4 Hippo | 9.0 | AD 6 Occipital Ctx | 19.5 |
| Control (Path) 3 Hippo | 6.7 | Control 1 Occipital Ctx | 5.8 |
| AD 1 Temporal Ctx | 11.2 | Control 2 Occipital Ctx | 83.5 |
| AD 2 Temporal Ctx | 37.6 | Control 3 Occipital Ctx | 19.3 |
| AD 3 Temporal Ctx | 4.0 | Control 4 Occipital Ctx | 5.0 |
| AD 4 Temporal Ctx | 21.5 | Control (Path) 1 Occipital Ctx | 88.9 |
| AD 5 Inf Temporal Ctx | 100.0 | Control (Path) 2 Occipital Ctx | 13.4 |
| AD 5 Sup Temporal Ctx | 37.9 | Control (Path) 3 Occipital Ctx | 5.8 |
| AD 6 Inf Temporal Ctx | 35.6 | Control (Path) 4 Occipital Ctx | 24.3 |
| AD 6 Sup Temporal Ctx | 39.2 | Control 1 Parietal Ctx | 9.4 |
| Control 1 Temporal Ctx | 6.7 | Control 2 Parietal Ctx | 44.4 |
| Control 2 Temporal Ctx | 65.5 | Control 3 Parietal Ctx | 28.5 |
| Control 3 Temporal Ctx | 19.3 | Control (Path) 1 Parietal Ctx | 90.8 |
| Control 3 Temporal Ctx | 11.4 | Control (Path) 2 Parietal Ctx | 25.7 |
| Control (Path) 1 Temporal Ctx | 83.5 | Control (Path) 3 Parietal Ctx | 5.6 |
| Control (Path) 2 Temporal Ctx | 56.6 | Control (Path) 4 Parietal Ctx | 56.6 |

Table AMC. General screening panel v1.4

| Issue Name | Run 217043912 | Issue Name | Run 217043912 |
|------------|---------------|-----------------|---------------|
| Adipose | 8.2 | Renal ca. TK-10 | 66.4 |

| | | | |
|----------------------------------|------|-------------------------------------|------|
| Melanoma* Hs688(A).T | 30.6 | Bladder | 11.2 |
| Melanoma* Hs688(B).T | 34.6 | Gastric ca. (liver met.) NCI-N87 | 15.3 |
| Melanoma* M14 | 27.0 | Gastric ca. KATO III | 20.6 |
| Melanoma* LOXIMVI | 17.6 | Colon ca. SW-948 | 1.1 |
| Melanoma* SK- MEL-5 | 25.3 | Colon ca. SW480 | 33.0 |
| Squamous cell carcinoma SCC-4 | 5.7 | Colon ca.* (SW480 met) SW620 | 29.9 |
| Testis Pool | 17.8 | Colon ca. HT29 | 8.8 |
| Prostate ca.* (bone met) PC-3 | 27.7 | Colon ca. HCT-116 | 15.4 |
| Prostate Pool | 16.0 | Colon ca. CaCo-2 | 13.1 |
| Placenta | 11.0 | Colon cancer tissue | 13.8 |
| Uterus Pool | 1.7 | Colon ca. SW1116 | 7.9 |
| Ovarian ca. OVCAR-3 | 17.0 | Colon ca. Colo-205 | 4.4 |
| Ovarian ca. SK-OV- 3 | 11.3 | Colon ca. SW-48 | 9.3 |
| Ovarian ca. OVCAR-4 | 7.1 | Colon Pool | 20.4 |
| Ovarian ca. OVCAR-5 | 37.4 | Small Intestine Pool | 12.5 |
| Ovarian ca. IGROV- 1 | 23.7 | Stomach Pool | 12.1 |
| Ovarian ca. OVCAR-8 | 16.8 | Bone Marrow Pool | 4.3 |
| Ovary | 20.0 | Fetal Heart | 18.7 |
| Breast ca. MCF-7 | 5.6 | Heart Pool | 12.3 |
| Breast ca. MDA- MB-231 | 41.5 | Lymph Node Pool | 18.9 |
| Breast ca. BT 549 | 55.1 | Fetal Skeletal Muscle | 8.9 |
| Breast ca. T47D | 63.3 | Skeletal Muscle Pool | 23.2 |
| Breast ca. MDA-N | 23.5 | Spleen Pool | 10.8 |
| Breast Pool | 25.5 | Thymus Pool | 18.0 |
| Trachea | 13.6 | CNS cancer (glio/astro) U87-MG | 62.4 |
| Lung | 5.3 | CNS cancer (glio/astro) | 12.5 |

| | | | |
|-------------------|-----|-------------------------------|------|
| Lung ca. NCI-N417 | 6.2 | CNS cancer (astro) SI- 539 | 17.3 |
|-------------------|-----|-------------------------------|------|

| | | | |
|-------------------|--------------|-------------------------------|------|
| Lung ca. LX-1 | 33.7 | CNS cancer (astro) SNB-75 | 27.2 |
| Lung ca. NCI-H146 | 10.0 | CNS cancer (glio) SNB-19 | 25.9 |
| Lung ca. SHP-77 | 39.2 | CNS cancer (glio) SF-295 | 54.0 |
| Lung ca. A549 | 43.8 | Brain (Amygdala) Pool | 47.6 |
| Lung ca. NCI-H526 | 6.5 | Brain (cerebellum) | 90.1 |
| Lung ca. NCI-H23 | 44.8 | Brain (fetal) | 56.6 |
| Lung ca. NCI-H460 | 23.8 | Brain (Hippocampus) Pool | 45.7 |
| Lung ca. HOP-62 | 53.6 | Cerebral Cortex Pool | 60.3 |
| Lung ca. NCI-H522 | 100.0 | Brain (Substantia nigra) Pool | 61.6 |
| Liver | 4.4 | Brain (Thalamus) Pool | 75.8 |
| Fetal Liver | 17.0 | Brain (whole) | 63.3 |
| Liver ca. HepG2 | 33.9 | Spinal Cord Pool | 24.1 |
| Kidney Pool | 37.1 | Adrenal Gland | 23.5 |
| Fetal Kidney | 16.4 | Pituitary gland Pool | 3.9 |
| Renal ca. 786-0 | 14.8 | Salivary Gland | 9.9 |
| Renal ca. A498 | 7.5 | Thyroid (female) | 29.1 |
| Renal ca. ACHN | 26.2 | Pancreatic ca. CAPAN2 | 39.8 |
| Renal ca. UO-31 | 81.8 | Pancreas Pool | 49.3 |

Table AMD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3387, Run 165296475 | Tissue Name | Rel. Exp.(%) Ag3387, Run 165296475 |
|--------------------|--|---|--|
| Secondary Th1 act | 24.1 | HUVEC IL-1beta | 12.1 |
| Secondary Th2 act | 29.9 | HUVEC IFN gamma | 27.0 |
| Secondary Tr1 act | 26.2 | HUVEC TNF alpha + IFN gamma | 19.1 |
| Secondary Th1 rest | 18.9 | HUVEC TNF alpha + IL4 | 16.0 |
| Secondary Th2 rest | 22.8 | HUVEC IL-11 | 16.4 |
| Secondary Tr1 rest | 28.1 | Lung Microvascular EC none | 36.6 |
| Primary Th1 act | 12.4 | Lung Microvascular EC TNFalpha + IL-1beta | 27.2 |

Microvascular Dermal EC

| Primary Th1 act | TNFalpha + IL-1beta |
|------------------|---------------------|
| Primary Th1 rest | 46.0 |

| | | TNFalpha + IL1beta | |
|--------------------------------|------|--|------|
| Primary Th2 rest | 36.1 | Small airway epithelium none | 3.9 |
| Primary Tr1 rest | 37.6 | Small airway epithelium TNFalpha + IL-1beta | 33.2 |
| CD45RA CD4 lymphocyte act | 5.7 | Coronery artery SMC rest | 19.6 |
| CD45RO CD4 lymphocyte act | 19.9 | Coronery artery SMC TNFalpha + IL-1beta | 12.7 |
| CD8 lymphocyte act | 16.2 | Astrocytes rest | 27.9 |
| Secondary CD8 lymphocyte rest | 11.3 | Astrocytes TNFalpha + IL-1beta | 21.8 |
| Secondary CD8 lymphocyte act | 12.3 | KU-812 (Basophil) rest | 7.6 |
| CD4 lymphocyte none | 5.7 | KU-812 (Basophil) PMA/ionomycin | 22.1 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 12.2 | CCD1106 (Keratinocytes) none | 12.0 |
| LAK cells rest | 19.2 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 19.3 |
| LAK cells IL-2 | 25.9 | Liver cirrhosis | 9.4 |
| LAK cells IL-2+IL-12 | 10.2 | Lupus kidney | 3.2 |
| LAK cells IL-2+IFN gamma | 26.4 | NCI-H292 none | 62.0 |
| LAK cells IL-2+ IL-18 | 21.2 | NCI-H292 IL-4 | 71.2 |
| LAK cells PMA/ionomycin | 4.2 | NCI-H292 IL-9 | 52.5 |
| NK Cells IL-2 rest | 21.2 | NCI-H292 IL-13 | 24.8 |
| Two Way MLR 3 day | 30.6 | NCI-H292 IFN gamma | 33.7 |
| Two Way MLR 5 day | 26.2 | HPAEC none | 27.7 |
| Two Way MLR 7 day | 16.8 | HPAEC TNF alpha + IL-1 beta | 12.6 |
| PBMC rest | 10.7 | Lung fibroblast none | 25.3 |
| PBMC PWM | 21.3 | Lung fibroblast TNF alpha + IL-1 beta | 12.1 |
| PBMC PHA-L | 25.5 | Lung fibroblast IL-4 | 48.0 |
| Ramos (B cell) none | 18.4 | Lung fibroblast IL-9 | 34.6 |
| Ramos (B cell) ionomycin | 68.3 | Lung fibroblast IL-13 | 51.1 |
| B lymphocytes PWM | 54.0 | Lung fibroblast IFN gamma | 63.3 |
| EOL-1 dbcAMP | 18.4 | Dermal fibroblast CCD1070 TNF alpha | 74.2 |

| | | | |
|-------------------------------|------|--|-------|
| EOL-1 dbcAMP PMA/ionomycin | 3.1 | Dermal fibroblast CCD1070 IL-1 beta | 4.6 |
| Dendritic cells none | 28.1 | Dermal fibroblast IFN gamma | 10.1 |
| Dendritic cells LPS | 29.7 | Dermal fibroblast IL-4 | 23.8 |
| Dendritic cells anti- CD40 | 19.6 | IBD Colitis 2 | 1.4 |
| Monocytes rest | 17.2 | IBD Crohn's | 2.4 |
| Monocytes LPS | 1.6 | Colon | 21.8 |
| Macrophages rest | 30.8 | Lung | 16.6 |
| Macrophages LPS | 17.4 | Thymus | 100.0 |
| HUVEC none | 22.8 | Kidney | 48.0 |
| HUVEC starved | 28.5 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3387 This panel does not show differential expression of the CG58662-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3387 Expression of the CG58662-01 gene is ubiquitous in this panel, with highest expression in a lung cancer cell line (CT=29.5). In addition, this gene is expressed at higher levels in kidney cancer cell lines when compared to normal kidney expression. Thus, expression of this gene could be used to differentiate these samples from other samples and as a marker for these cancers. Furthermore, therapeutic modulation of the expression of function of this gene may be effective in the treatment of lung and kidney cancer.

Among metabolic tissues this gene is expressed at moderate to low levels in adipose, adrenal gland, pancreas, pituitary, and adult and fetal skeletal muscle, heart and liver. This widespread expression among these tissues suggests that this gene plays a role in normal metabolic and neuroendocrine function and that disregulated expression of this gene may contribute to neuroendocrine diseases or metabolic disorders, such as obesity and diabetes.

In addition, this gene is expressed at moderate to low levels in all CNS regions examined and may be a small molecule target for the treatment of neurologic diseases, such

Panel 4D Summary: Ag3387 The CG58662-01 gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease, with highest expression in the thymus (CT=31). In addition, expression is seen in members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.5 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AN. CG59371-01: Novel cytoplasmic protein

Expression of gene CG59371-01 was assessed using the primer-probe set Ag3558, described in Table ANA. Results of the RTQ-PCR runs are shown in Tables ANB, ANC, AND and ANE.

Table ANA. Probe Name Ag3558

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' -cttgaggctgagaaggagaag-3' | 21 | 208 | 517 |
| Probe | TET -5' -tgcttatcaactcacagagaaggaca -3' -TAMRA | 26 | 231 | 518 |
| Reverse | 5' -gttggtctctcagtcgcgtgt -3' | 21 | 263 | 519 |

Table ANB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3558, Run 213391281 | Tissue Name | Rel. Exp.(%) Ag3558, Run 213391281 |
|-------------|---------------------------------------|----------------|---------------------------------------|
| Adipose | 0.4 | Renal ca TK-10 | 14.3 |

| | | | |
|------------------------|-----|------------------------------|-----|
| Melanoma Hs688(B).T | 5.2 | Gastric ca AGS/TK NCI-N87 | 5.2 |
|------------------------|-----|------------------------------|-----|

| | | | |
|-------------------------------|-------|-------------------------------------|------|
| Melanoma* M14 | 41.5 | Gastric ca. KATO III | 82.9 |
| Melanoma* LOXIMVI | 30.1 | Colon ca. SW-948 | 14.8 |
| Melanoma* SK-MEL-5 | 23.8 | Colon ca. SW480 | 81.2 |
| Squamous cell carcinoma SCC-4 | 34.6 | Colon ca.* (SW480 met) SW620 | 24.0 |
| Testis Pool | 7.6 | Colon ca. HT29 | 20.6 |
| Prostate ca.* (bone met) PC-3 | 9.7 | Colon ca. HCT-116 | 61.6 |
| Prostate Pool | 0.1 | Colon ca. CaCo-2 | 17.7 |
| Placenta | 0.3 | Colon cancer tissue | 7.7 |
| Uterus Pool | 0.1 | Colon ca. SW1116 | 6.9 |
| Ovarian ca. OVCAR-3 | 15.3 | Colon ca. Colo-205 | 3.2 |
| Ovarian ca. SK-OV-3 | 62.0 | Colon ca. SW-48 | 9.3 |
| Ovarian ca. OVCAR-4 | 27.5 | Colon Pool | 0.3 |
| Ovarian ca. OVCAR-5 | 14.4 | Small Intestine Pool | 0.1 |
| Ovarian ca. IGROV-1 | 5.8 | Stomach Pool | 2.0 |
| Ovarian ca. OVCAR-8 | 2.5 | Bone Marrow Pool | 0.3 |
| Ovary | 0.2 | Fetal Heart | 3.3 |
| Breast ca. MCF-7 | 15.5 | Heart Pool | 0.0 |
| Breast ca. MDA-MB-231 | 100.0 | Lymph Node Pool | 0.5 |
| Breast ca. BT 549 | 72.7 | Fetal Skeletal Muscle | 0.7 |
| Breast ca. T47D | 17.1 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 13.5 | Spleen Pool | 0.8 |
| Breast Pool | 0.2 | Thymus Pool | 7.2 |
| Trachea | 0.4 | CNS cancer (glio/astro) U87-MG | 17.6 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 61.6 |
| Fetal Lung | 2.5 | CNS cancer (neuro;met) SK-N-AS | 14.9 |
| Lung ca. NCI-N417 | 5.4 | CNS cancer (astro) SF- | 21.6 |

| | | | |
|-------------------|------|-----------------------------|-----|
| Lung ca. NCI-H146 | 15.2 | CNS cancer (glio) SNB-19 | 4.6 |
|-------------------|------|-----------------------------|-----|

| | | | |
|-------------------|------|-------------------------------|------|
| Lung ca. SHP-77 | 42.0 | CNS cancer (glio) SF-295 | 0.8 |
| Lung ca. A549 | 28.5 | Brain (Amygdala) Pool | 0.1 |
| Lung ca. NCI-H526 | 6.4 | Brain (cerebellum) | 0.0 |
| Lung ca. NCI-H23 | 21.3 | Brain (fetal) | 1.1 |
| Lung ca. NCI-H460 | 0.7 | Brain (Hippocampus) Pool | 0.2 |
| Lung ca. HOP-62 | 4.7 | Cerebral Cortex Pool | 0.1 |
| Lung ca. NCI-H522 | 23.8 | Brain (Substantia nigra) Pool | 0.1 |
| Liver | 0.0 | Brain (Thalamus) Pool | 0.0 |
| Fetal Liver | 0.8 | Brain (whole) | 0.0 |
| Liver ca. HepG2 | 7.7 | Spinal Cord Pool | 0.1 |
| Kidney Pool | 0.1 | Adrenal Gland | 0.2 |
| Fetal Kidney | 4.1 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 52.5 | Salivary Gland | 0.0 |
| Renal ca. A498 | 6.5 | Thyroid (female) | 0.2 |
| Renal ca. ACHN | 14.0 | Pancreatic ca. CAPAN2 | 43.2 |
| Renal ca. UO-31 | 20.2 | Pancreas Pool | 0.9 |

Table ANC. General screening panel v1.5

| Tissue Name | Rel. Exp.(%) Ag3558, Run 248592792 | Tissue Name | Rel. Exp.(%) Ag3558, Run 248592792 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 0.4 | Renal ca. TK-10 | 16.6 |
| Melanoma* Hs688(A).T | 2.0 | Bladder | 3.3 |
| Melanoma* Hs688(B).T | 3.1 | Gastric ca. (liver met.) NCI-N87 | 6.7 |
| Melanoma* M14 | 34.9 | Gastric ca. KATO III | 93.3 |
| Melanoma* LOXIMVI | 26.4 | Colon ca. SW-948 | 13.0 |
| Melanoma* SK-MEL-5 | 29.5 | Colon ca. SW480 | 76.3 |
| Squamous cell carcinoma SCC-4 | 33.0 | Colon ca.* (SW480 met) SW620 | 25.5 |
| Testis Pool | 7.2 | Colon ca. HT29 | 18.8 |
| Prostate ca.* (bone met) PC-3 | 10.3 | Colon ca. HCT-116 | 55.5 |

Dose: 100 µg/ml; Incubation time: 1 hr; Detection: 24 hr

| | | |
|-------------|---------------|--------------------|
| uterus Pool | Colo ca. D543 | Colon ca. Colo-205 |
| Ovarian ca. | 29.5 | 5.6 |

| OVCAR-3 | | | |
|-----------------------|--------------|-------------------------------------|------|
| Ovarian ca. SK-OV-3 | 40.6 | Colon ca. SW-48 | 6.8 |
| Ovarian ca. OVCAR-4 | 29.5 | Colon Pool | 0.2 |
| Ovarian ca. OVCAR-5 | 11.7 | Small Intestine Pool | 0.2 |
| Ovarian ca. IGROV-1 | 4.6 | Stomach Pool | 0.2 |
| Ovarian ca. OVCAR-8 | 5.2 | Bone Marrow Pool | 0.2 |
| Ovary | 0.2 | Fetal Heart | 2.0 |
| Breast ca. MCF-7 | 18.0 | Heart Pool | 0.0 |
| Breast ca. MDA-MB-231 | 85.3 | Lymph Node Pool | 0.5 |
| Breast ca. BT 549 | 100.0 | Fetal Skeletal Muscle | 0.8 |
| Breast ca. T47D | 23.3 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 20.2 | Spleen Pool | 1.0 |
| Breast Pool | 0.3 | Thymus Pool | 3.7 |
| Trachea | 0.4 | CNS cancer (glio/astro) U87-MG | 15.4 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 64.6 |
| Fetal Lung | 3.5 | CNS cancer (neuro;met) SK-N-AS | 24.7 |
| Lung ca. NCI-N417 | 5.0 | CNS cancer (astro) SF-539 | 21.6 |
| Lung ca. LX-1 | 32.1 | CNS cancer (astro) SNB-75 | 30.4 |
| Lung ca. NCI-H146 | 13.6 | CNS cancer (glio) SNB-19 | 4.8 |
| Lung ca. SHP-77 | 34.9 | CNS cancer (glio) SF-295 | 3.3 |
| Lung ca. A549 | 35.4 | Brain (Amygdala) Pool | 0.0 |
| Lung ca. NCI-H526 | 3.4 | Brain (cerebellum) | 0.0 |
| Lung ca. NCI-H23 | 15.9 | Brain (fetal) | 0.7 |
| Lung ca. NCI-H460 | 0.4 | Brain (Hippocampus) Pool | 0.0 |
| Lung ca. HOP-62 | 4.5 | Cerebral Cortex Pool | 0.0 |
| Lung ca. NCI-H522 | 25.5 | Brain (Substantia nigra) pool | 0.0 |
| Liver ca. HepG2 | 6.6 | Brain (whole) Spinal Cord Pool | 0.0 |

| | | | |
|-----------------|------|-----------------------|------|
| Kidney Pool | 0.1 | Adrenal Gland | 0.1 |
| Fetal Kidney | 4.6 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 44.1 | Salivary Gland | 0.0 |
| Renal ca. A498 | 4.2 | Thyroid (female) | 0.1 |
| Renal ca. ACHN | 15.2 | Pancreatic ca. CAPAN2 | 48.3 |
| Renal ca. UO-31 | 20.4 | Pancreas Pool | 0.5 |

Table AND. Panel 2.2

| Tissue Name | Rel. Exp.(%) Ag3558, Run 173762113 | Rel. Exp.(%) Ag3558, Run 174924057 | Tissue Name | Rel. Exp.(%) Ag3558, Run 173762113 | Rel. Exp.(%) Ag3558, Run 174924057 |
|---|--|--|--|--|--|
| Normal Colon | 12.5 | 5.6 | Kidney Margin (OD04348) | 3.3 | 1.1 |
| Colon cancer (OD06064) | 100.0 | 100.0 | Kidney malignant cancer (OD06204B) | 5.6 | 8.9 |
| Colon Margin (OD06064) | 27.5 | 17.7 | Kidney normal adjacent tissue (OD06204E) | 0.6 | 0.3 |
| Colon cancer (OD06159) | 3.1 | 4.8 | Kidney Cancer (OD04450-01) | 6.3 | 2.8 |
| Colon Margin (OD06159) | 5.6 | 7.3 | Kidney Margin (OD04450-03) | 0.6 | 0.0 |
| Colon cancer (OD06297-04) | 11.5 | 16.6 | Kidney Cancer 8120613 | 0.0 | 0.0 |
| Colon Margin (OD06297-05) | 12.5 | 7.8 | Kidney Margin 8120614 | 0.3 | 0.3 |
| CC Gr.2 ascend colon (ODO3921) | 6.9 | 5.7 | Kidney Cancer 9010320 | 0.2 | 1.9 |
| CC Margin (ODO3921) | 6.8 | 6.4 | Kidney Margin 9010321 | 2.1 | 2.3 |
| Colon cancer metastasis (OD06104) | 6.8 | 4.9 | Kidney Cancer 8120607 | 0.8 | 1.7 |
| Lung Margin (OD06104) | 17.9 | 12.6 | Kidney Margin 8120608 | 0.3 | 0.0 |
| Colon mets to lung (OD04451- | 15.1 | 23.3 | Normal Uterus | 1.6 | 0.5 |

| | | | | | |
|-----------------|-----|-----|----------------|-----|-----|
| Normal Prostate | 2.1 | 0.0 | Normal Thyroid | 0.3 | 0.0 |
|-----------------|-----|-----|----------------|-----|-----|

| | | | | | |
|---|------|------|---|------|------|
| Prostate Cancer (OD04410) | 0.0 | 0.2 | Thyroid Cancer 064010 | 1.1 | 0.7 |
| Prostate Margin (OD04410) | 0.4 | 0.3 | Thyroid Cancer A302152 | 1.2 | 1.0 |
| Normal Ovary | 2.7 | 0.4 | Thyroid Margin A302153 | 0.3 | 0.3 |
| Ovarian cancer (OD06283-03) | 30.1 | 32.8 | Normal Breast | 2.7 | 1.9 |
| Ovarian Margin (OD06283-07) | 1.4 | 1.3 | Breast Cancer (OD04566) | 7.4 | 8.5 |
| Ovarian Cancer 064008 | 7.0 | 1.9 | Breast Cancer 1024 | 4.3 | 6.5 |
| Ovarian cancer (OD06145) | 1.2 | 1.9 | Breast Cancer (OD04590-01) | 11.8 | 13.9 |
| Ovarian Margin (OD06145) | 0.9 | 0.6 | Breast Cancer Mets (OD04590-03) | 8.0 | 6.8 |
| Ovarian cancer (OD06455-03) | 28.1 | 30.4 | Breast Cancer Metastasis (OD04655-05) | 7.9 | 11.0 |
| Ovarian Margin (OD06455-07) | 0.7 | 0.6 | Breast Cancer 064006 | 5.7 | 5.8 |
| Normal Lung | 1.4 | 1.3 | Breast Cancer 9100266 | 0.7 | 0.3 |
| Invasive poor diff. lung adeno (ODO4945-01) | 25.0 | 20.3 | Breast Margin 9100265 | 1.8 | 1.1 |
| Lung Margin (ODO4945-03) | 1.0 | 1.7 | Breast Cancer A209073 | 2.5 | 1.2 |
| Lung Malignant Cancer (OD03126) | 6.3 | 6.4 | Breast Margin A2090734 | 3.0 | 1.2 |
| Lung Margin (OD03126) | 1.3 | 1.0 | Breast cancer (OD06083) | 15.7 | 24.7 |
| Lung Cancer (OD05014A) | 13.5 | 10.3 | Breast cancer node metastasis (OD06083) | 16.5 | 15.0 |
| Lung Margin (OD05014B) | 3.1 | 4.8 | Normal Liver | 0.0 | 0.0 |
| Lung cancer (OD06081) | 38.4 | 28.7 | Liver Cancer 1026 | 1.2 | 0.0 |
| Lung Margin | | | Liver Cancer | . | . |

| | | | | | |
|-------------|-----|-----|--------------|-----|-----|
| Lung Margin | 0.8 | 1.9 | Liver Tissue | 2.2 | 1.4 |
|-------------|-----|-----|--------------|-----|-----|

| | | | | | |
|---------------------------------------|------|------|------------------------|------|------|
| (OD04237-02) | | | 6004-N | | |
| Ocular Melanoma Metastasis | 0.2 | 0.6 | Liver Cancer 6005-T | 0.8 | 1.0 |
| Ocular Melanoma Margin (Liver) | 0.0 | 0.0 | Liver Tissue 6005-N | 1.3 | 0.3 |
| Melanoma Metastasis | 13.2 | 12.5 | Liver Cancer 064003 | 1.6 | 2.0 |
| Melanoma Margin (Lung) | 1.6 | 1.1 | Normal Bladder | 4.4 | 4.4 |
| Normal Kidney | 0.3 | 0.0 | Bladder Cancer 1023 | 4.6 | 1.9 |
| Kidney Ca, Nuclear grade 2 (OD04338) | 0.0 | 1.0 | Bladder Cancer A302173 | 23.0 | 15.4 |
| Kidney Margin (OD04338) | 0.8 | 0.3 | Normal Stomach | 6.5 | 9.5 |
| Kidney Ca Nuclear grade 1/2 (OD04339) | 0.6 | 2.6 | Gastric Cancer 9060397 | 2.9 | 3.2 |
| Kidney Margin (OD04339) | 0.8 | 0.6 | Stomach Margin 9060396 | 4.9 | 1.0 |
| Kidney Ca, Clear cell type (OD04340) | 0.6 | 1.2 | Gastric Cancer 9060395 | 6.3 | 4.6 |
| Kidney Margin (OD04340) | 0.7 | 1.4 | Stomach Margin 9060394 | 3.5 | 3.0 |
| Kidney Ca, Nuclear grade 3 (OD04348) | 36.9 | 31.0 | Gastric Cancer 064005 | 22.1 | 20.0 |

Table ANE. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3558, Run 166488678 | Tissue Name | Rel. Exp.(%) Ag3558, Run 166488678 |
|-------------------|--|-----------------------|--|
| Secondary Th1 act | 17.9 | HUVEC IL-1beta | 10.3 |
| Secondary Th2 act | 12.4 | HUVEC IFN gamma | 12.2 |
| | | HUVEC TNF alpha + IFN | |

| | | | |
|--------------------|-----|-----------------------|-----|
| Secondary Th1 rest | | HUVEC IL-1beta | |
| Secondary Th1 rest | 2.5 | Lung Microvascular EC | 5.2 |

| | | | |
|---------------------------------|------|--|------|
| | | none | |
| Primary Th1 act | 9.1 | Lung Microvascular EC TNFalpha + IL-1beta | 4.8 |
| Primary Th2 act | 11.6 | Microvascular Dermal EC none | 19.5 |
| Primary Tr1 act | 11.4 | Microvascular Dermal EC TNFalpha + IL-1beta | 8.5 |
| Primary Th1 rest | 32.8 | Bronchial epithelium TNFalpha + IL1beta | 1.0 |
| Primary Th2 rest | 10.4 | Small airway epithelium none | 0.5 |
| Primary Tr1 rest | 13.4 | Small airway epithelium TNFalpha + IL-1beta | 5.8 |
| CD45RA CD4 lymphocyte act | 10.7 | Coronery artery SMC rest | 2.3 |
| CD45RO CD4 lymphocyte act | 17.2 | Coronery artery SMC TNFalpha + IL-1beta | 1.3 |
| CD8 lymphocyte act | 12.2 | Astrocytes rest | 1.4 |
| Secondary CD8 lymphocyte rest | 11.7 | Astrocytes TNFalpha + IL-1beta | 0.7 |
| Secondary CD8 lymphocyte act | 10.4 | KU-812 (Basophil) rest | 3.1 |
| CD4 lymphocyte none | 0.1 | KU-812 (Basophil) PMA/ionomycin | 6.6 |
| 2ry Th1/Th2/Tr1_ anti-CD95 CH11 | 6.0 | CCD1106 (Keratinocytes) none | 11.3 |
| LAK cells rest | 1.8 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 2.6 |
| LAK cells IL-2 | 16.3 | Liver cirrhosis | 0.3 |
| LAK cells IL-2+IL-12 | 9.7 | Lupus kidney | 0.0 |
| LAK cells IL-2+IFN gamma | 19.9 | NCI-H292 none | 12.2 |
| LAK cells IL-2+ IL-18 | 16.4 | NCI-H292 IL-4 | 29.7 |
| LAK cells PMA/ionomycin | 0.7 | NCI-H292 IL-9 | 24.3 |
| NK Cells IL-2 rest | 9.9 | NCI-H292 IL-13 | 16.4 |
| Two Way MLR 3 day | 1.5 | NCI-H292 IFN gamma | 16.0 |
| Two Way MLR 5 day | 7.4 | HPAEC none | 8.9 |
| Two Way MLR 7 day | 6.1 | HPAEC TNF alpha + IL-1 beta | 5.5 |

DD 8/17/02 . . . Lung fibroblast none . . . 2.2

| | | | |
|---------------------|------|----------------------|------|
| PBMC PHA-L | 23.5 | Lung fibroblast IL-4 | 16.8 |
| Ramos (B cell) none | 13.4 | Lung fibroblast IL-9 | 2.3 |

| | | | |
|------------------------------|------|-------------------------------------|-------|
| Ramos (B cell) ionomycin | 47.0 | Lung fibroblast IL-13 | 0.5 |
| B lymphocytes PWM | 79.0 | Lung fibroblast IFN gamma | 0.5 |
| B lymphocytes CD40L and IL-4 | 16.2 | Dermal fibroblast CCD1070 rest | 48.6 |
| EOL-1 dbcAMP | 6.3 | Dermal fibroblast CCD1070 TNF alpha | 100.0 |
| EOL-1 dbcAMP PMA/ionomycin | 4.5 | Dermal fibroblast CCD1070 IL-1 beta | 25.5 |
| Dendritic cells none | 1.1 | Dermal fibroblast IFN gamma | 14.0 |
| Dendritic cells LPS | 0.1 | Dermal fibroblast IL-4 | 14.9 |
| Dendritic cells anti-CD40 | 0.1 | IBD Colitis 2 | 0.5 |
| Monocytes rest | 0.0 | IBD Crohn's | 0.2 |
| Monocytes LPS | 0.0 | Colon | 1.7 |
| Macrophages rest | 3.0 | Lung | 1.2 |
| Macrophages LPS | 0.4 | Thymus | 0.0 |
| HUVEC none | 18.7 | Kidney | 11.4 |
| HUVEC starved | 0.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3558 Expression of the CG59371-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3558 Highest expression of the CG59371-01 gene is seen in a breast cancer cell line (CT=23.4). Overall, expression of this gene is significantly higher in cancer cell lines and fetal derived tissues than in samples derived from normal adult tissues. There are significant levels of expression in clusters of cell lines derived from pancreatic, brain, colon, gastric, renal, lung, ovarian, breast and melanoma cancers. Thus, expression of this gene could be used to differentiate between the cancer derived samples and fetal tissues from other samples on this panel and as a marker to detect the presence of cancer. Furthermore, the much higher levels of expression in proliferative tissue suggest that this gene may be involved in cell proliferation. Therefore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

Among tissues with metabolic function this gene is expressed at moderate to low

levels in heart, liver, and lung. The widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that deregulated

expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This molecule is a novel protein phosphatase expressed at moderate to low levels in all regions of the CNS examined. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

General_screening_panel_v1.5 Summary: Ag3558 Results from this experiment are in excellent agreement with results from Panel 1.4. Please see that panel for discussion of utility of this gene in cancer, metabolic disorders and the central nervous system.

Panel 2.2 Summary: Ag3558 Two experiments with the same probe and primer produce results that are in excellent agreement, with highest expression of the CG59371-01 gene in colon cancer (CTs=30). Furthermore, expression is higher in kidney, lung, ovary and colon cancers when compared to normal adjacent tissue. In addition, significant expression is also seen in gastric, breast, and bladder cancer. Thus, , expression of this gene in could be used to differentiate between the cancer derived samples and other samples on this panel and as a marker to detect the presence of cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

Panel 4D Summary: Ag3558 The CG59371-01 gene is widely expressed among the samples on this panel, with highest expression in dermal fibroblasts treated with TNF-alpha. Significant levels of expression are also seen in treated and untreated samples from skin, lung, T-cells and B-cells. Therefore, modulation of the expression or activity of the protein encoded by this transcript through the application of antibodies or peptides therapeutics may be beneficial for the treatment of lung inflammatory diseases such as asthma, and chronic obstructive pulmonary diseases, inflammatory skin diseases such as psoriasis, atopic dermatitis, ulcerative dermatitis, and ulcerative colitis, autoimmune diseases such as Crohn's disease, lupus erythematosus, rheumatoid arthritis and osteoarthritis and in other diseases in which T cells and B cells are activated.

Expression of gene CG59346-01 was assessed using the primer-probe set Ag3550, described in Table AOA. Results of the RTQ-PCR runs are shown in Tables AOB, AOC and AOD.

Table AOA. Probe Name Ag3550

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -gcacaacagagatgaacaaagag-3' | 22 | 3459 | 520 |
| Probe | TET-5' -accgcctctccttcccgctct-3' -TAMRA | 23 | 3508 | 521 |
| Reverse | 5' -ttggaaggctaaagacatctga-3' | 22 | 3532 | 522 |

Table AOB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3550, Run 210641081 | Tissue Name | Rel. Exp.(%) Ag3550, Run 210641081 |
|---------------------------|---------------------------------------|-----------------------------------|---------------------------------------|
| AD 1 Hippo | 12.8 | Control (Path) 3 Temporal Ctx | 5.1 |
| AD 2 Hippo | 38.7 | Control (Path) 4 Temporal Ctx | 40.3 |
| AD 3 Hippo | 10.4 | AD 1 Occipital Ctx | 18.8 |
| AD 4 Hippo | 15.8 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 Hippo | 79.6 | AD 3 Occipital Ctx | 7.2 |
| AD 6 Hippo | 49.3 | AD 4 Occipital Ctx | 25.9 |
| Control 2 Hippo | 37.4 | AD 5 Occipital Ctx | 37.6 |
| Control 4 Hippo | 10.3 | AD 6 Occipital Ctx | 19.6 |
| Control (Path) 3 Hippo | 9.6 | Control 1 Occipital Ctx | 2.1 |
| AD 1 Temporal Ctx | 15.7 | Control 2 Occipital Ctx | 56.6 |
| AD 2 Temporal Ctx | 37.1 | Control 3 Occipital Ctx | 26.8 |
| AD 3 Temporal Ctx | 8.6 | Control 4 Occipital Ctx | 5.0 |
| AD 4 Temporal Ctx | 30.6 | Control (Path) 1 Occipital Ctx | 93.3 |
| AD 5 Inf Temporal Ctx | 66.9 | Control (Path) 2 Occipital Ctx | 14.6 |

| | | | |
|--------------------------|------|-----------------------------------|------|
| AD 5 Inf Temporal Ctx | 66.9 | Control (Path) 2 Occipital Ctx | 14.6 |
|--------------------------|------|-----------------------------------|------|

| | | | |
|-------------------------------|-------|-------------------------------|------|
| AD 6 Sup Temporal Ctx | 53.2 | Control 1 Parietal Ctx | 8.7 |
| Control 1 Temporal Ctx | 7.3 | Control 2 Parietal Ctx | 48.0 |
| Control 2 Temporal Ctx | 36.6 | Control 3 Parietal Ctx | 17.2 |
| Control 3 Temporal Ctx | 29.7 | Control (Path) 1 Parietal Ctx | 84.1 |
| Control 3 Temporal Ctx | 14.6 | Control (Path) 2 Parietal Ctx | 28.5 |
| Control (Path) 1 Temporal Ctx | 100.0 | Control (Path) 3 Parietal Ctx | 4.6 |
| Control (Path) 2 Temporal Ctx | 65.5 | Control (Path) 4 Parietal Ctx | 56.6 |

Table AOC_General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3550, Run 217048931 | Tissue Name | Rel. Exp.(%) Ag3550, Run 217048931 |
|-------------------------------|------------------------------------|----------------------------------|------------------------------------|
| Adipose | 0.5 | Renal ca. TK-10 | 27.7 |
| Melanoma* Hs688(A).T | 1.4 | Bladder | 13.7 |
| Melanoma* Hs688(B).T | 1.6 | Gastric ca. (liver met.) NCI-N87 | 25.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 24.5 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 1.4 |
| Melanoma* SK-MEL-5 | 0.8 | Colon ca. SW480 | 8.8 |
| Squamous cell carcinoma SCC-4 | 2.1 | Colon ca.* (SW480 met) SW620 | 7.4 |
| Testis Pool | 2.0 | Colon ca. HT29 | 2.0 |
| Prostate ca.* (bone met) PC-3 | 15.2 | Colon ca. HCT-116 | 7.1 |
| Prostate Pool | 6.7 | Colon ca. CaCo-2 | 92.0 |
| Placenta | 18.9 | Colon cancer tissue | 6.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 1.8 |
| Ovarian ca. OVCAR-3 | 7.6 | Colon ca. Colo-205 | 3.0 |
| Ovarian ca. SK-OV-3 | 14.9 | Colon ca. SW-48 | 3.1 |

| | | | |
|--------------------|------|----------------------|-----|
| Ovarian ca OVCAR-5 | 24.5 | Small Intestine Pool | 5.0 |
|--------------------|------|----------------------|-----|

| | | | |
|-----------------------|------|-------------------------------------|-------|
| Ovarian ca. IGROV-1 | 2.1 | Stomach Pool | 6.9 |
| Ovarian ca. OVCAR-8 | 2.4 | Bone Marrow Pool | 0.2 |
| Ovary | 1.4 | Fetal Heart | 0.1 |
| Breast ca. MCF-7 | 34.6 | Heart Pool | 0.1 |
| Breast ca. MDA-MB-231 | 8.2 | Lymph Node Pool | 2.8 |
| Breast ca. BT 549 | 0.2 | Fetal Skeletal Muscle | 0.2 |
| Breast ca. T47D | 57.4 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 1.8 |
| Breast Pool | 4.6 | Thymus Pool | 7.2 |
| Trachea | 14.1 | CNS cancer (glio/astro) U87-MG | 0.1 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.1 |
| Fetal Lung | 19.5 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 1.5 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 24.7 | CNS cancer (astro) SNB-75 | 0.0 |
| Lung ca. NCI-H146 | 7.4 | CNS cancer (glio) SNB-19 | 2.1 |
| Lung ca. SHP-77 | 0.2 | CNS cancer (glio) SF-295 | 0.1 |
| Lung ca. A549 | 26.1 | Brain (Amygdala) Pool | 22.1 |
| Lung ca. NCI-H526 | 13.9 | Brain (cerebellum) | 63.3 |
| Lung ca. NCI-H23 | 6.6 | Brain (fetal) | 100.0 |
| Lung ca. NCI-H460 | 11.1 | Brain (Hippocampus) Pool | 28.1 |
| Lung ca. HOP-62 | 0.2 | Cerebral Cortex Pool | 34.2 |
| Lung ca. NCI-H522 | 0.5 | Brain (Substantia nigra) Pool | 26.2 |
| Liver | 3.6 | Brain (Thalamus) Pool | 37.9 |
| Fetal Liver | 19.1 | Brain (whole) | 57.8 |
| Liver ca. HepG2 | 26.4 | Spinal Cord Pool | 2.8 |
| Kidney Pool | 0.3 | Adrenal Gland | 2.6 |
| Fetal Kidney | 11.7 | Pituitary gland Pool | 3.6 |
| Renal ca. 786-0 | 23.3 | Salivary Gland | 25.5 |

Renal ca. 786-0

Pancreas Pool

Table AOD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3550, Run 166453850 | Tissue Name | Rel. Exp.(%) Ag3550, Run 166453850 |
|--------------------------------|--|---|--|
| Secondary Th1 act | 0.2 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 0.1 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 0.0 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 0.0 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 0.0 |
| Primary Tr1 act | 0.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 9.5 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 8.1 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 27.2 |
| CD45RA CD4 lymphocyte act | 1.4 | Coronery artery SMC rest | 0.7 |
| CD45RO CD4 lymphocyte act | 0.0 | Coronery artery SMC TNFalpha + IL-1beta | 1.0 |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 5.2 |
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 5.9 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.1 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 10.5 |
| LAK cells rest | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 23.0 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 22.8 |

| | | |
|-----------------------|---------------|------|
| gamma | NCI-H292 IL-4 | 81.8 |
| LAK cells IL-2+ IL-18 | 0.0 | |

| | | | |
|-------------------------------|------|---------------------------------------|-------|
| LAK cells PMA/ionomycin | 0.0 | NCI-H292 IL-9 | 69.7 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 58.6 |
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 61.1 |
| Two Way MLR 5 day | 0.0 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 57.4 |
| PBMC PWM | 0.0 | Lung fibroblast TNF alpha + IL-1 beta | 45.7 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 36.6 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 33.9 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 17.2 |
| B lymphocytes PWM | 2.4 | Lung fibroblast IFN gamma | 34.9 |
| B lymphocytes CD40L and IL-4 | 11.3 | Dermal fibroblast CCD1070 rest | 28.5 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 11.3 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 4.8 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 0.3 |
| Dendritic cells LPS | 0.0 | Dermal fibroblast IL-4 | 0.0 |
| Dendritic cells anti-CD40 | 0.3 | IBD Colitis 2 | 6.9 |
| Monocytes rest | 36.3 | IBD Crohn's | 2.0 |
| Monocytes LPS | 0.0 | Colon | 36.6 |
| Macrophages rest | 0.0 | Lung | 14.3 |
| Macrophages LPS | 0.0 | Thymus | 100.0 |
| HUVEC none | 0.0 | Kidney | 0.1 |
| HUVEC starved | 0.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3550 This panel does not show differential expression of the CG59346-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.4 for discussion of utility of this gene in the central nervous system.

cerebral cortex, and thalamus and at moderate levels in the amygdala, hippocampus, and

thalamus. This CG59346-01 gene encodes a homologue of Proline-rich synapse-associated protein-1/cortactin binding protein 1 (ProSAP1/CortBP1). ProSAP1 is PDZ-domain protein highly enriched in the postsynaptic density (PSD) and involved in the assembly of the PSD during neuronal differentiation that may function with cortactin, in the recruitment and activation of neural intracellular signaling pathways. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

In addition, moderate levels of expression are seen in colon, gastric, renal, pancreatic, lung, ovarian, breast and prostate cancer cell lines. Thus, expression of this gene could be used to detect the presence of cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that deregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

In addition, this gene is expressed at higher levels in fetal lung and kidney (CTs=29) when compared to expression in adult lung and kidney (CTs=35-40). Thus, expression of this gene could be used to differentiate between the two sources of lung and kidney tissue.

References:

1. Peles E, Nativ M, Lustig M, Grumet M, Schilling J, Martinez R, Plowman GD, Schlessinger J. Identification of a novel cortactin-associated transmembrane receptor with multiple domains implicated in protein-protein interactions. *EMBO J* 1997 Mar 3;16(5):978-88.
2. Boeckers TM, Kreutz MR, Winter C, Zuschratter W, Smalla KH, Sanmarti-Vila L, Wex H, Langnaese K, Bockmann J, Garner CC, Gundelfinger ED. (1999) Proline-rich synapse-associated protein-1/cortactin binding protein 1 (ProSAP1/CortBP1) is a PDZ-domain

Panel 4D Summary: Ag3550 Highest expression of the CG59346-01 gene is seen in thymus (CT=27). In addition, significant levels of expression are seen in IL-4, IL-9, IL-13 and IFN gamma activated-NCI-H292 mucoepidermoid cells as well as untreated NCI-H292 cells. Moderate/low expression is also detected in IL-4, IL-9, IL-13 and IFN gamma activated lung fibroblasts, small airway epithelium (treated and untreated), and treated bronchial epithelium. The expression of this gene in cells derived from or within the lung suggests that this gene may be involved in normal conditions as well as pathological and inflammatory lung disorders that include chronic obstructive pulmonary disease, asthma, allergy and emphysema.

In addition, significant levels of expression are seen in treated and untreated dermal fibroblasts and keratinocytes, suggesting that modulation of the expression or function of this gene may also reduce symptoms in inflammatory skin diseases such as psoriasis, atopic dermatitis, and ulcerative dermatitis.

AP. CG57814-01 and CG57814-02: Basic I 19 protein

Expression of gene CG57814-01 and variant CG57814-02 was assessed using the primer-probe set Ag791, described in Table APA.

Table APA. Probe Name Ag791

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-aaatgtgatgaccaaggttctg-3' | 22 | 1290 | 523 |
| Probe | TET-5'-agcacacattatccagcgaaagcatg-3' - TAMRA | 26 | 1319 | 524 |
| Reverse | 5'-tgtcaaagaacccttggtc-3' | 22 | 1368 | 525 |

Panel 1.2 Summary: Ag791 Expression of the CG57814-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

AQ. CG59327-01: MONOCARBOXYLATE TRANSPORTER 1 like protein

Expression of gene CG59327-01 was assessed using the primer-probe set Ag3548, described in Table AQA. Results of the RTQ-PCR runs are shown in Tables AQB and AQC.

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|-----------|--------|----------------|------------|
|---------|-----------|--------|----------------|------------|

| | | | | |
|---------|---|----|-----|-----|
| Forward | 5'-atttgcatacagcagctttgtc-3' | 22 | 517 | 526 |
| Probe | TET-5'-ttcatctcccagaaatcgtaattg-3' - TAMRA | 26 | 549 | 527 |
| Reverse | 5'-accttcgttgctccaataagt-3' | 22 | 579 | 528 |

Table AQB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3548, Run 217048438 | Tissue Name | Rel. Exp.(%) Ag3548, Run 217048438 |
|----------------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 0.0 | Renal ca. TK-10 | 3.6 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 0.0 |
| Melanoma* Hs688(B).T | 0.0 | Gastric ca. (liver met.) NCI-N87 | 0.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 0.0 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |
| Melanoma* SK-MEL-5 | 0.0 | Colon ca. SW480 | 1.3 |
| Squamous cell carcinoma SCC-4 | 0.0 | Colon ca.* (SW480 met) SW620 | 0.0 |
| Testis Pool | 0.0 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 0.0 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 0.0 |
| Placenta | 0.0 | Colon cancer tissue | 0.0 |
| Uterus Pool | 1.2 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.0 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.0 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.0 | Colon Pool | 2.2 |
| Ovarian ca. OVCAR-5 | 0.0 | Small Intestine Pool | 0.0 |
| Ovarian ca. IGROV-1 | 0.0 | Stomach Pool | 0.0 |
| Ovarian ca. OVCAR-8 | 0.0 | Bone Marrow Pool | 0.0 |
| Ovary | 0.0 | Fetal Heart | 0.0 |
| Breast ca. MCF-7 | 0.0 | Heart Pool | 0.0 |

Breast ca. BT-549 Fetal Brain Fetal Skeletal Muscle

| | | | |
|-------------------|-------|-------------------------------------|-----|
| Breast ca. T47D | 0.0 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 0.0 |
| Breast Pool | 0.0 | Thymus Pool | 0.0 |
| Trachea | 0.0 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 2.4 | CNS cancer (glio/astro) U-118-MG | 6.5 |
| Fetal Lung | 0.0 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF- 539 | 0.0 |
| Lung ca. LX-1 | 0.0 | CNS cancer (astro) SNB-75 | 6.4 |
| Lung ca. NCI-H146 | 0.0 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 0.0 | CNS cancer (glio) SF- 295 | 0.0 |
| Lung ca. A549 | 0.0 | Brain (Amygdala) Pool | 0.0 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 0.0 |
| Lung ca. NCI-H23 | 0.0 | Brain (fetal) | 0.0 |
| Lung ca. NCI-H460 | 0.0 | Brain (Hippocampus) Pool | 0.0 |
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 0.0 |
| Lung ca. NCI-H522 | 3.1 | Brain (Substantia nigra) Pool | 0.0 |
| Liver | 0.0 | Brain (Thalamus) Pool | 0.0 |
| Fetal Liver | 0.0 | Brain (whole) | 0.0 |
| Liver ca. HepG2 | 0.0 | Spinal Cord Pool | 0.0 |
| Kidney Pool | 0.0 | Adrenal Gland | 0.0 |
| Fetal Kidney | 3.4 | Pituitary gland Pool | 0.0 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 0.0 |
| Renal ca. A498 | 100.0 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 0.0 |
| Renal ca. UO-31 | 0.0 | Pancreas Pool | 0.0 |

Table AQC. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3548, Run 166453848 | Tissue Name | Rel. Exp.(%) Ag3548, Run 166453848 |
|-------------------|--|--------------------------------|--|
| Secondary Tr1 act | 0.0 | HUVEC TNF alpha + IFN gamma | 0.0 |

| | | | |
|--------------------------------|-----|---|--------------|
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.5 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 0.0 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 100.0 |
| Primary Tr1 act | 0.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 0.2 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 1.2 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 0.0 | Coronery artery SMC rest | 0.0 |
| CD45RO CD4 lymphocyte act | 0.0 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 0.3 |
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 0.0 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.3 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 0.0 |
| LAK cells rest | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 6.5 |
| LAK cells IL-2+IL-12 | 0.0 | Lupus kidney | 0.7 |
| LAK cells IL-2+IFN gamma | 0.0 | NCI-H292 none | 1.8 |
| LAK cells IL-2+ IL-18 | 0.0 | NCI-H292 IL-4 | 1.7 |
| LAK cells PMA/ionomycin | 0.0 | NCI-H292 IL-9 | 0.2 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 0.0 |
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 0.0 |
| Total WMLR 5 day | 0.0 | HPAEc none | 0.5 |

| | | | |
|-----------|-----|---------------------------|-----|
| PBMC rest | 0.0 | Lung fibroblast none | 0.0 |
| PBMC PWM | 0.0 | Lung fibroblast TNF alpha | 0.0 |

| | | + IL-1 beta | |
|---------------------------------|-----|--|-----|
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 0.0 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 0.0 |
| B lymphocytes PWM | 0.0 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 rest | 0.0 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 0.0 | Dermal fibroblast IL-4 | 0.0 |
| Dendritic cells anti- CD40 | 0.0 | IBD Colitis 2 | 2.0 |
| Monocytes rest | 0.0 | IBD Crohn's | 3.5 |
| Monocytes LPS | 0.0 | Colon | 1.0 |
| Macrophages rest | 0.0 | Lung | 2.3 |
| Macrophages LPS | 0.0 | Thymus | 0.7 |
| HUVEC none | 0.0 | Kidney | 0.0 |
| HUVEC starved | 0.4 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3548 Expression of the CG59327-01 gene is low/undetectable in all the samples on the panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3548 Significant expression of the CG59327-01 gene is restricted to a sample derived from a kidney cancer cell line (CT=33.34). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of kidney cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of kidney cancer.

Panel 4D Summary: Ag3548 Significant expression of the CG59327-01 gene is restricted to a samples derived from untreated microvascular dermal endothelial cells (CT=30.3). Thus,

Expression of gene CG59494-01, which represents a full length physical clone, was assessed using the primer-probe set Ag3206, described in Table ARA. Results of the RTQ-PCR runs are shown in Tables ARB and ARC.

Table ARA. Probe Name Ag3206

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -agtgttcatggaaaatgtga-3' | 22 | 160 | 455 |
| Probe | TET-5' -ccataagaacagaaagtctttccaggaca-3' -TAMRA | 30 | 182 | 758 |
| Reverse | 5' -ccccagcttgaaggagatc-3' | 19 | 216 | 759 |

Table ARB. Panel 1.3D

| Tissue Name | Rel. Exp.(%) Ag3206, Run 165527079 | Tissue Name | Rel. Exp.(%) Ag3206, Run 165527079 |
|--------------------------|------------------------------------|--------------------------------|------------------------------------|
| Liver adenocarcinoma | 0.0 | Kidney (fetal) | 10.5 |
| Pancreas | 0.0 | Renal ca. 786-0 | 0.0 |
| Pancreatic ca. CAPAN 2 | 17.8 | Renal ca. A498 | 15.6 |
| Adrenal gland | 0.0 | Renal ca. RXF 393 | 0.0 |
| Thyroid | 0.0 | Renal ca. ACHN | 14.8 |
| Salivary gland | 0.0 | Renal ca. UO-31 | 0.0 |
| Pituitary gland | 0.0 | Renal ca. TK-10 | 0.0 |
| Brain (fetal) | 0.0 | Liver | 0.0 |
| Brain (whole) | 9.9 | Liver (fetal) | 0.0 |
| Brain (amygdala) | 0.0 | Liver ca. (hepatoblast) HepG2 | 0.0 |
| Brain (cerebellum) | 0.0 | Lung | 0.0 |
| Brain (hippocampus) | 0.0 | Lung (fetal) | 0.0 |
| Brain (substantia nigra) | 0.0 | Lung ca. (small cell) LX-1 | 4.5 |
| Brain (thalamus) | 0.0 | Lung ca. (small cell) NCI-H69 | 0.0 |
| Cerebral Cortex | 0.0 | Lung ca. (s.cell var.) SHP-77 | 18.0 |
| Spinal cord | 33.4 | Lung ca. (large cell) NCI-H460 | 41.2 |

| | | | |
|--------------------------------|------|-----------------------------------|-------|
| astrocytoma SW1783 | 0.0 | Lung ca. (non-s.cell) HOP-62 | 0.0 |
| neuro*; met SK-N-AS | 0.0 | Lung ca. (non-s.cl) NCI-H522 | 0.0 |
| astrocytoma SF-539 | 0.0 | Lung ca. (squam.) SW 900 | 0.0 |
| astrocytoma SNB-75 | 11.7 | Lung ca. (squam.) NCI-H596 | 0.0 |
| glioma SNB-19 | 0.0 | Mammary gland | 14.4 |
| glioma U251 | 0.0 | Breast ca.* (pl.ef) MCF-7 | 0.0 |
| glioma SF-295 | 0.0 | Breast ca.* (pl.ef) MDA-MB-231 | 0.0 |
| Heart (fetal) | 0.0 | Breast ca.* (pl.ef) T47D | 0.0 |
| Heart | 15.5 | Breast ca. BT-549 | 0.0 |
| Skeletal muscle (fetal) | 0.0 | Breast ca. MDA-N | 0.0 |
| Skeletal muscle | 0.0 | Ovary | 0.0 |
| Bone marrow | 0.0 | Ovarian ca. OVCAR-3 | 14.0 |
| Thymus | 0.0 | Ovarian ca. OVCAR-4 | 0.0 |
| Spleen | 0.0 | Ovarian ca. OVCAR-5 | 0.0 |
| Lymph node | 0.0 | Ovarian ca. OVCAR-8 | 0.0 |
| Colorectal | 0.0 | Ovarian ca. IGROV-1 | 11.6 |
| Stomach | 0.0 | Ovarian ca.* (ascites) SK-OV-3 | 0.0 |
| Small intestine | 0.0 | Uterus | 0.0 |
| Colon ca. SW480 | 0.0 | Placenta | 0.0 |
| Colon ca.* SW620(SW480 met) | 0.0 | Prostate | 0.0 |
| Colon ca. HT29 | 0.0 | Prostate ca.* (bone met)PC-3 | 100.0 |
| Colon ca. HCT-116 | 0.0 | Testis | 27.5 |
| Colon ca. CaCo-2 | 42.0 | Melanoma Hs688(A).T | 0.0 |
| Colon ca. tissue(ODO3866) | 0.0 | Melanoma* (met) Hs688(B).T | 0.0 |

| NCI NS | Metabolism | Metabolism |
|---------|------------|--------------|
| Bladder | 0.0 | Melanoma LOX |

| | | IMVI | |
|---------|-----|-----------------------------|-----|
| Trachea | 0.0 | Melanoma* (met) SK-MEL-5 | 0.0 |
| Kidney | 0.0 | Adipose | 0.0 |

Table ARC, Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3206, Run 164531735 | Tissue Name | Rel. Exp.(%) Ag3206, Run 164531735 |
|-------------------------------|--|---|--|
| Secondary Th1 act | 0.0 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 11.9 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 0.0 | HUVEC TNF alpha + IFN gamma | 12.6 |
| Secondary Th1 rest | 11.9 | HUVEC TNF alpha + IL4 | 15.9 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 75.8 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 100.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 72.2 |
| Primary Tr1 act | 0.0 | Microvasular Dermal EC TNFalpha + IL1beta | 0.0 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 0.0 |
| Primary Th2 rest | 0.0 | Small airway epithelium none | 0.0 |
| Primary Tr1 rest | 0.0 | Small airway epithelium TNFalpha + IL-1beta | 0.0 |
| CD45RA CD4 lymphocyte act | 0.0 | Coronery artery SMC rest | 0.0 |
| CD45RO CD4 lymphocyte act | 0.0 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 0.0 |
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 0.0 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.0 |
| LAK cells rest | 0.0 | CD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |

| | | | |
|------------------------------|------|---------------------------------------|------|
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 29.7 |
| LAK cells IL-2+IL-12 | 0.0 | Lupus kidney | 0.0 |
| LAK cells IL-2+IFN gamma | 0.0 | NCI-H292 none | 97.3 |
| LAK cells IL-2+ IL-18 | 0.0 | NCI-H292 IL-4 | 0.0 |
| LAK cells PMA/ionomycin | 0.0 | NCI-H292 IL-9 | 43.8 |
| NK Cells IL-2 rest | 7.8 | NCI-H292 IL-13 | 24.0 |
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 12.7 |
| Two Way MLR 5 day | 0.0 | HPAEC none | 14.3 |
| Two Way MLR 7 day | 0.0 | HPAEC TNF alpha + IL-1 beta | 33.2 |
| PBMC rest | 0.0 | Lung fibroblast none | 0.0 |
| PBMC PWM | 0.0 | Lung fibroblast TNF alpha + IL-1 beta | 0.0 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 16.2 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 15.9 |
| B lymphocytes PWM | 0.0 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 rest | 0.0 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.0 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |
| Dendritic cells none | 0.0 | Dermal fibroblast IFN gamma | 0.0 |
| Dendritic cells LPS | 0.0 | Dermal fibroblast IL-4 | 15.0 |
| Dendritic cells anti-CD40 | 0.0 | IBD Colitis 2 | 27.4 |
| Monocytes rest | 0.0 | IBD Crohn's | 0.0 |
| Monocytes LPS | 0.0 | Colon | 6.7 |
| Macrophages rest | 0.0 | Lung | 0.0 |
| Macrophages LPS | 0.0 | Thymus | 0.0 |
| HUVEC none | 27.7 | Kidney | 0.0 |
| HUVEC starved | 20.0 | | |

Panel 1.3D Summary: Ag3206 Expression of the CG59494-01 gene is restricted to a sample

able to differentiate between the samples with other samples (e.g., IBD, Crohn's disease, etc.)

detect the presence of prostate cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of prostate cancer.

Panel 4D Summary: Ag3206 Expression of the CG59494-01 gene is primarily restricted to a cluster of samples derived from microvasculature of the lung and the dermis suggesting a role for this gene in the maintenance of the integrity of the microvasculature. Therefore, therapeutics designed for this putative protein could be beneficial for the treatment of diseases associated with damaged microvasculature including heart diseases or inflammatory diseases, such as psoriasis, asthma, and chronic obstructive pulmonary diseases.

AS. CG59432-01 and CG59432-02: Chloride Channel

Expression of gene CG59432-01 and CG59432-02 was assessed using the primer-probe set Ag5938, described in Table ASA. Results of the RTQ-PCR runs are shown in Tables ASB and ASC. Please note that CG59432-02 represents a full-length physical clone of CG59432-01 gene, validating the prediction of the gene sequence.

Table ASA. Probe Name Ag5938

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---------------------------------------|--------|----------------|------------|
| Forward | 5'-tttgtgtcagtctataccattaa-3' | 22 | 626 | 529 |
| Probe | TET-5'-accagcttggcctgtccagt-3' -TAMRA | 22 | 658 | 530 |
| Reverse | 5'-tcctggagttcagagtatatct-3' | 22 | 710 | 531 |

Table ASB. General_screening_panel_v1.5

| Tissue Name | Rel. Exp.(%) Ag5938, Run 248102142 | Tissue Name | Rel. Exp.(%) Ag5938, Run 248102142 |
|-------------------------|---------------------------------------|-------------------------------------|---------------------------------------|
| Adipose | 6.3 | Renal ca. TK-10 | 2.7 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 17.6 |
| Melanoma* Hs688(B).T | 0.0 | Gastric ca. (liver met.) NCI-N87 | 100.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 8.2 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |

| | | | |
|----------------------------------|------|----------------------------------|-----|
| Squamous cell carcinoma SCC-4 | 21.5 | Colon ca * (SW480) met) SW620 | 0.6 |
|----------------------------------|------|----------------------------------|-----|

| | | | |
|-------------------------------|------|-------------------------------------|------|
| Testis Pool | 21.0 | Colon ca. HT29 | 7.1 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 11.0 |
| Prostate Pool | 6.9 | Colon ca. CaCo-2 | 25.2 |
| Placenta | 0.0 | Colon cancer tissue | 4.7 |
| Uterus Pool | 1.5 | Colon ca. SW1116 | 2.7 |
| Ovarian ca. OVCAR-3 | 20.2 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.0 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.0 | Colon Pool | 5.7 |
| Ovarian ca. OVCAR-5 | 24.7 | Small Intestine Pool | 7.6 |
| Ovarian ca. IGROV-1 | 0.0 | Stomach Pool | 3.2 |
| Ovarian ca. OVCAR-8 | 2.8 | Bone Marrow Pool | 6.6 |
| Ovary | 0.0 | Fetal Heart | 1.0 |
| Breast ca. MCF-7 | 4.2 | Heart Pool | 4.3 |
| Breast ca. MDA-MB-231 | 0.0 | Lymph Node Pool | 3.8 |
| Breast ca. BT 549 | 0.0 | Fetal Skeletal Muscle | 59.9 |
| Breast ca. T47D | 0.0 | Skeletal Muscle Pool | 93.3 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 3.2 |
| Breast Pool | 10.4 | Thymus Pool | 3.6 |
| Trachea | 15.1 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 0.6 | CNS cancer (glio/astro) U-118-MG | 3.1 |
| Fetal Lung | 31.6 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 0.0 | CNS cancer (astro) SNB-75 | 0.0 |
| Lung ca. NCI-H146 | 3.2 | CNS cancer (glio) SNB-19 | 3.6 |
| Lung ca. SHP-77 | 0.0 | CNS cancer (glio) SF-295 | 0.0 |

| | | | |
|--------------------|-----|----------------------------|------|
| Lung ca. A549 | 0.0 | Brain (Acampeptidyl Pept.) | 17.2 |
| Lung ca. NCI-H1295 | 0.0 | Brain (Cellular) | 0.0 |
| Lung ca. NCI-H460 | 0.0 | Brain (Hippocampus) | 15.8 |

| | | Pool | |
|-------------------|------|-------------------------------|------|
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 27.0 |
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) Pool | 25.2 |
| Liver | 0.0 | Brain (Thalamus) Pool | 29.1 |
| Fetal Liver | 7.0 | Brain (whole) | 9.5 |
| Liver ca. HepG2 | 0.0 | Spinal Cord Pool | 11.0 |
| Kidney Pool | 6.8 | Adrenal Gland | 8.4 |
| Fetal Kidney | 17.1 | Pituitary gland Pool | 6.3 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 4.8 |
| Renal ca. A498 | 0.0 | Thyroid (female) | 0.0 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 1.4 |
| Renal ca. UO-31 | 0.0 | Pancreas Pool | 4.5 |

Table ASC. Panel 5 Islet

| Tissue Name | Rel. Exp.(%) Ag5938, Run 248045753 | Tissue Name | Rel. Exp.(%) Ag5938, Run 248045753 |
|------------------------------------|--|--|--|
| 97457_Patient-02go_adipose | 0.0 | 94709_Donor 2 AM - A_adipose | 0.0 |
| 97476_Patient-07sk_skeletal muscle | 0.0 | 94710_Donor 2 AM - B_adipose | 0.0 |
| 97477_Patient-07ut_uterus | 0.0 | 94711_Donor 2 AM - C_adipose | 0.0 |
| 97478_Patient-07pl_placenta | 1.1 | 94712_Donor 2 AD - A_adipose | 0.0 |
| 99167_Bayer Patient 1 | 0.0 | 94713_Donor 2 AD - B_adipose | 0.0 |
| 97482_Patient-08ut_uterus | 0.0 | 94714_Donor 2 AD - C_adipose | 0.0 |
| 97483_Patient-08pl_placenta | 0.0 | 94742_Donor 3 U - A_Mesenchymal Stem Cells | 0.0 |
| 97486_Patient-09sk_skeletal muscle | 0.0 | 94743_Donor 3 U - B_Mesenchymal Stem Cells | 0.0 |
| 97487_Patient-09ut_uterus | 0.0 | 94730_Donor 3 AM - A_adipose | 0.7 |
| 97488_Patient-09pl_placenta | 0.5 | 94731_Donor 3 AM - B_adipose | 0.0 |
| 97492_Patient-10ut_uterus | 0.0 | 94732_Donor 3 AM - C_adipose | 0.0 |

97498_Patient-11go_adipose 94734_Donor 3 AD - B_adipose

| | | | |
|--|-----|---|-------|
| 97496_Patient-11sk_skeletal muscle | 2.4 | 94735_Donor 3 AD - C_adipose | 0.0 |
| 97497_Patient-11ut_uterus | 0.0 | 77138_Liver_HepG2untreated | 0.0 |
| 97498_Patient-11pl_placenta | 0.0 | 73556_Heart_Cardiac stromal cells (primary) | 0.0 |
| 97500_Patient-12go_adipose | 0.7 | 81735_Small Intestine | 100.0 |
| 97501_Patient-12sk_skeletal muscle | 6.8 | 72409_Kidney_Proximal Convoluted Tubule | 0.0 |
| 97502_Patient-12ut_uterus | 0.0 | 82685_Small intestine_Duodenum | 4.6 |
| 97503_Patient-12pl_placenta | 0.0 | 90650_Adrenal_Adrenocortical adenoma | 0.0 |
| 94721_Donor 2 U - A_Mesenchymal Stem Cells | 0.0 | 72410_Kidney_HRCE | 0.0 |
| 94722_Donor 2 U - B_Mesenchymal Stem Cells | 0.0 | 72411_Kidney_HRE | 0.0 |
| 94723_Donor 2 U - C_Mesenchymal Stem Cells | 6.5 | 73139_Uterus_Uterine smooth muscle cells | 0.0 |

General_screening_panel_v1.5 Summary: Ag5938 Highest expression of the CG59432-01 gene is seen in a gastric cancer cell line (CT=32.5). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel. In addition, low expression of this gene is seen in colon cancer CaCo-2, lung cancer NCI-H526, ovarian cancer OVCAR-5, and squamous cell carcinoma SCC-4 cell lines. Therefore, therapeutic modulation of the activity of this gene or its protein product, through the use of small molecule drugs, protein therapeutics or antibodies, might be beneficial in the treatment of these cancers.

Significant expression is also detected in fetal skeletal muscle and adult skeletal muscle (CT=32.5). At least 50 disease-causing mutations in the skeletal muscle voltage-gated chloride channel gene (CLCN1), almost all of which originate from Caucasian families, have been identified. Therefore, therapeutic modulation of this gene product, a chloride channel homolog, may be a treatment for myotonia congenita and other muscle channelopathies.

Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

References:

1. Sasaki R, Ito N, Shimamura M, Murakami T, Kuzuhara S, Uchino M, Uyama E. A novel CLCN1 mutation: P480T in a Japanese family with Thomsen's myotonia congenita. Muscle Nerve. 2001 Mar;24(3):357-63.

Panel 5 Islet Summary: Ag5938 Expression of the CG59432-01 is restricted to a sample from small intestine (CT=31.6). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker for this tissue.

AT. CG59383-01: D6MM5E

Expression of gene CG59383-01 was assessed using the primer-probe set Ag3427, described in Table ATA. Results of the RTQ-PCR runs are shown in Tables ATB, ATC and ATD.

Table ATA. Probe Name Ag3427

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' -cagtggAACAGACCAAGAAC-3' | 21 | 784 | 532 |
| Probe | TET-5' -tctttcttcacagtgttcagcaaca-3' - TAMRA | 26 | 817 | 533 |
| Reverse | 5' -ggattatctctgggtctggaa-3' | 21 | 844 | 534 |

Table ATB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3427, Run 210351187 | Tissue Name | Rel. Exp.(%) Ag3427, Run 210351187 |
|-------------|---------------------------------------|----------------------------------|---------------------------------------|
| AD 1 Hippo | 11.4 | Control (Path) 3 Temporal Ctx | 2.0 |
| AD 2 Hippo | 50.3 | Control (Path) 4 Temporal Ctx | 23.3 |
| AD 3 Hippo | 10.2 | AD 1 Occipital Ctx | 9.8 |

| | | | |
|------------|------|--------------------|------|
| AD 5 Hippo | 42.9 | AD 5 Occipital Ctx | 17.0 |
| AD 6 Hippo | | AD 4 Occipital Ctx | |

| | | | |
|-------------------------------|-------|--------------------------------|------|
| Control 2 Hippo | 21.2 | AD 5 Occipital Ctx | 25.3 |
| Control 4 Hippo | 6.1 | AD 6 Occipital Ctx | 29.9 |
| Control (Path) 3 Hippo | 15.1 | Control 1 Occipital Ctx | 3.0 |
| AD 1 Temporal Ctx | 22.7 | Control 2 Occipital Ctx | 32.3 |
| AD 2 Temporal Ctx | 45.1 | Control 3 Occipital Ctx | 26.2 |
| AD 3 Temporal Ctx | 6.0 | Control 4 Occipital Ctx | 8.4 |
| AD 4 Temporal Ctx | 39.0 | Control (Path) 1 Occipital Ctx | 84.1 |
| AD 5 Inf Temporal Ctx | 100.0 | Control (Path) 2 Occipital Ctx | 11.7 |
| AD 5 Sup Temporal Ctx | 53.6 | Control (Path) 3 Occipital Ctx | 0.9 |
| AD 6 Inf Temporal Ctx | 57.0 | Control (Path) 4 Occipital Ctx | 10.3 |
| AD 6 Sup Temporal Ctx | 58.2 | Control 1 Parietal Ctx | 6.4 |
| Control 1 Temporal Ctx | 18.8 | Control 2 Parietal Ctx | 48.6 |
| Control 2 Temporal Ctx | 51.1 | Control 3 Parietal Ctx | 38.7 |
| Control 3 Temporal Ctx | 16.5 | Control (Path) 1 Parietal Ctx | 54.7 |
| Control 3 Temporal Ctx | 5.5 | Control (Path) 2 Parietal Ctx | 8.4 |
| Control (Path) 1 Temporal Ctx | 82.9 | Control (Path) 3 Parietal Ctx | 1.4 |
| Control (Path) 2 Temporal Ctx | 33.0 | Control (Path) 4 Parietal Ctx | 16.2 |

Table ATC_General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3427, Run 216821480 | Tissue Name | Rel. Exp.(%) Ag3427, Run 216821480 |
|-------------------------|---------------------------------------|--------------------------|---------------------------------------|
| Adipose | 0.5 | Renal ca. TK-10 | 8.4 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 1.7 |
| Melanoma* | | Gastric ca. (liver met.) | |
| Metanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |

| | | | |
|-------------------------------|------|----------------------------------|-------|
| Melanoma* SK-MEL-5 | 0.2 | Colon ca. SW480 | 0.4 |
| Squamous cell carcinoma SCC-4 | 14.5 | Colon ca.* (SW480 met) SW620 | 0.1 |
| Testis Pool | 10.7 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 100.0 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 0.1 |
| Placenta | 0.2 | Colon cancer tissue | 1.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 2.9 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 50.7 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 2.1 | Colon Pool | 0.4 |
| Ovarian ca. OVCAR-5 | 1.1 | Small Intestine Pool | 0.3 |
| Ovarian ca. IGROV-1 | 9.7 | Stomach Pool | 0.9 |
| Ovarian ca. OVCAR-8 | 13.7 | Bone Marrow Pool | 0.4 |
| Ovary | 0.2 | Fetal Heart | 0.0 |
| Breast ca. MCF-7 | 0.1 | Heart Pool | 0.0 |
| Breast ca. MDA-MB-231 | 0.0 | Lymph Node Pool | 0.4 |
| Breast ca. BT 549 | 0.0 | Fetal Skeletal Muscle | 0.2 |
| Breast ca. T47D | 2.1 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 0.2 |
| Breast Pool | 1.7 | Thymus Pool | 1.4 |
| Trachea | 1.7 | CNS cancer (glio/astro) U87-MG | 0.0 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.4 |
| Fetal Lung | 0.4 | CNS cancer (neuro;met) SK-N-AS | 0.1 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 0.3 | CNS cancer (astro) SNB-75 | 0.8 |

| Lung ca. A549 | | NS cancer (astro) | |
|---------------|--|-------------------|--|
| | | 295 | |

| | | | |
|-------------------|-----|-------------------------------|-----|
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 0.9 |
| Lung ca. NCI-H23 | 0.2 | Brain (fetal) | 0.1 |
| Lung ca. NCI-H460 | 0.0 | Brain (Hippocampus) Pool | 2.2 |
| Lung ca. HOP-62 | 0.5 | Cerebral Cortex Pool | 1.7 |
| Lung ca. NCI-H522 | 0.1 | Brain (Substantia nigra) Pool | 1.0 |
| Liver | 0.0 | Brain (Thalamus) Pool | 2.9 |
| Fetal Liver | 0.1 | Brain (whole) | 1.7 |
| Liver ca. HepG2 | 0.0 | Spinal Cord Pool | 0.2 |
| Kidney Pool | 0.2 | Adrenal Gland | 0.4 |
| Fetal Kidney | 0.8 | Pituitary gland Pool | 1.3 |
| Renal ca. 786-0 | 0.1 | Salivary Gland | 0.6 |
| Renal ca. A498 | 0.1 | Thyroid (female) | 1.9 |
| Renal ca. ACHN | 0.0 | Pancreatic ca. CAPAN2 | 0.1 |
| Renal ca. UO-31 | 0.5 | Pancreas Pool | 2.3 |

Table ATD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3427, Run 166396769 | Tissue Name | Rel. Exp.(%) Ag3427, Run 166396769 |
|--------------------|--|--|--|
| Secondary Th1 act | 1.4 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 0.0 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 0.8 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 1.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 2.9 | Lung Microvascular EC none | 0.0 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 0.0 |
| Primary Tr1 act | 4.9 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.0 |
| Primary Th1 rest | 2.5 | Bronchial epithelium TNFalpha + IL1beta | 7.9 |
| Primary Th2 rest | 2.0 | Small airway epithelium none | 0.0 |

| | | | |
|---------------------------|-----|--------------------------|-----|
| CD45RA CD4 lymphocyte act | 0.0 | Coronery artery SMC rest | 0.0 |
|---------------------------|-----|--------------------------|-----|

| | | | |
|--------------------------------|-----|---|-------|
| CD45RO CD4 lymphocyte act | 0.9 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 5.0 |
| Secondary CD8 lymphocyte rest | 1.0 | Astrocytes TNFalpha + IL-1beta | 2.4 |
| Secondary CD8 lymphocyte act | 0.8 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.0 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 2.0 | CCD1106 (Keratinocytes) none | 28.5 |
| LAK cells rest | 0.0 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 100.0 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 23.8 |
| LAK cells IL-2+IL-12 | 1.6 | Lupus kidney | 3.4 |
| LAK cells IL-2+IFN gamma | 3.7 | NCI H292 none | 1.8 |
| LAK cells IL-2+ IL-18 | 0.9 | NCI-H292 IL-4 | 3.8 |
| LAK cells PMA/ionomycin | 0.0 | NCI-H292 IL-9 | 2.0 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 4.0 |
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 1.1 |
| Two Way MLR 5 day | 0.0 | HPAEC none | 0.0 |
| Two Way MLR 7 day | 0.9 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 0.0 |
| PBMC PWM | 0.7 | Lung fibroblast TNF alpha + IL-1 beta | 0.8 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 0.7 |
| Ramos (B cell) ionomycin | 0.0 | Lung fibroblast IL-13 | 0.0 |
| B lymphocytes PWM | 3.4 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 4.0 | Dermal fibroblast CCD1070 rest | 0.9 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 5.6 |
| EOL-1 dbcAMP PMA/ionomycin | 1.1 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |

| Dendritic cells anti-CD40 | 0.0 | Rectal epithelial cells IBD Colitis 2 | 5.9 |
|---------------------------|-----|---------------------------------------|-----|
|---------------------------|-----|---------------------------------------|-----|

| | | | |
|------------------|-----|-------------|------|
| Monocytes rest | 0.0 | IBD Crohn's | 2.4 |
| Monocytes LPS | 0.0 | Colon | 4.1 |
| Macrophages rest | 0.0 | Lung | 1.7 |
| Macrophages LPS | 0.0 | Thymus | 12.4 |
| HUVEC none | 0.0 | Kidney | 10.2 |
| HUVEC starved | 0.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3427 This panel confirms the expression of CG59383-01 gene at low levels in the brains of an independent group of individuals.

However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3427 Highest expression of the CG59383-01 gene is seen in a colon cancer cell line (CT=27.2). Significant expression is also seen in a cluster of samples derived from ovarian cancer cell lines. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker for the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of ovarian or colon cancers.

This molecule is also expressed at low levels in all regions of the CNS examined. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Among tissues with metabolic function, this gene is expressed at low levels in adipose and pancreas. This expression suggests that this gene product may play a role in normal neuroendocrine and metabolic and that disregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

Panel 4D Summary: Ag3427 Highest expression of the CG59383-01 gene is seen in keratinocytes treated with the inflammatory cytokines TNF-alpha and IL-1 beta (CT=30.3).

AU. CG58526-01: Scramblase

Expression of gene CG58526-01 was assessed using the primer-probe set Ag3366, described in Table AUA. Results of the RTQ-PCR runs are shown in Table AUB.

Table AUA. Probe Name Ag3366

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5'-tgtcttcacaaatgctgacaat-3' | 22 | 729 | 535 |
| Probe | TET-5'-ttcggaattcatgttcctgcagatct-3' TAMRA | 26 | 751 | 536 |
| Reverse | 5'-gatcattgctgcttgactgtt-3' | 22 | 783 | 537 |

Table AUB. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3366, Run 217042585 | Tissue Name | Rel. Exp.(%) Ag3366, Run 217042585 |
|-------------------------------|------------------------------------|----------------------------------|------------------------------------|
| Adipose | 0.0 | Renal ca. TK-10 | 0.0 |
| Melanoma* Hs688(A).T | 0.0 | Bladder | 0.0 |
| Melanoma* Hs688(B).T | 0.0 | Gastric ca. (liver met.) NCI-N87 | 0.0 |
| Melanoma* M14 | 0.0 | Gastric ca. KATO III | 0.0 |
| Melanoma* LOXIMVI | 0.0 | Colon ca. SW-948 | 0.0 |
| Melanoma* SK-MEL-5 | 0.0 | Colon ca. SW480 | 0.0 |
| Squamous cell carcinoma SCC-4 | 0.0 | Colon ca.* (SW480 met) SW620 | 100.0 |
| Testis Pool | 69.3 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.0 | Colon ca. HCT-116 | 25.2 |
| Prostate Pool | 0.0 | Colon ca. CaCo-2 | 43.2 |
| Placenta | 0.0 | Colon cancer tissue | 0.0 |
| Uterus Pool | 0.0 | Colon ca. SW1116 | 0.0 |
| Ovarian ca. OVCAR-3 | 0.0 | Colon ca. Colo-205 | 0.0 |
| Ovarian ca. SK-OV-3 | 0.0 | Colon ca. SW-48 | 0.0 |

| | | | |
|---------------------|---|----------------------|---|
| Variants OVCAR-3 | + | Small Intestine Pool | + |
|---------------------|---|----------------------|---|

| | | | |
|-----------------------|-----|-------------------------------------|------|
| Ovarian ca. IGROV-1 | 0.0 | Stomach Pool | 49.0 |
| Ovarian ca. OVCAR-8 | 0.0 | Bone Marrow Pool | 0.0 |
| Ovary | 0.0 | Fetal Heart | 0.0 |
| Breast ca. MCF-7 | 0.0 | Heart Pool | 0.0 |
| Breast ca. MDA-MB-231 | 0.0 | Lymph Node Pool | 0.0 |
| Breast ca. BT 549 | 0.0 | Fetal Skeletal Muscle | 0.0 |
| Breast ca. T47D | 0.0 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 0.0 | Spleen Pool | 3.9 |
| Breast Pool | 0.0 | Thymus Pool | 0.0 |
| Trachea | 0.0 | CNS cancer (glio/astro) U87-MG | 3.5 |
| Lung | 0.0 | CNS cancer (glio/astro) U-118-MG | 0.0 |
| Fetal Lung | 0.0 | CNS cancer (neuro;met) SK-N-AS | 0.0 |
| Lung ca. NCI-N417 | 0.0 | CNS cancer (astro) SF-539 | 0.0 |
| Lung ca. LX-1 | 0.0 | CNS cancer (astro) SNB-75 | 0.0 |
| Lung ca. NCI-H146 | 0.0 | CNS cancer (glio) SNB-19 | 0.0 |
| Lung ca. SHP-77 | 0.0 | CNS cancer (glio) SF-295 | 0.0 |
| Lung ca. A549 | 0.0 | Brain (Amygdala) Pool | 12.5 |
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 0.0 |
| Lung ca. NCI-H23 | 0.0 | Brain (fetal) | 13.8 |
| Lung ca. NCI-H460 | 0.0 | Brain (Hippocampus) Pool | 15.0 |
| Lung ca. HOP-62 | 0.0 | Cerebral Cortex Pool | 2.6 |
| Lung ca. NCI-H522 | 0.0 | Brain (Substantia nigra) Pool | 7.5 |
| Liver | 0.0 | Brain (Thalamus) Pool | 15.7 |
| Fetal Liver | 0.0 | Brain (whole) | 15.2 |
| Liver ca. HepG2 | 0.0 | Spinal Cord Pool | 7.5 |
| Kidney Pool | 0.0 | Adrenal Gland | 0.0 |
| Fetal Kidney | 0.0 | Pituitary gland Pool | 22.8 |
| Renal ca. 786-0 | 0.0 | Salivary Gland | 0.0 |

Renal ca. 786-0

Pancreas Pool

CNS_neurodegeneration_v1.0 Summary: Ag3366 Expression of the CG58526-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3366 Expression of the CG58526-01 gene is restricted to a sample derived from a colon cancer cell line (CT=34.5) and the testis. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of colon cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon cancer.

Panel 4D Summary: Ag3366 Results from one experiment with the CG58526-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

AV. CG57851-01: sulfotransferase

Expression of gene CG57851-01 was assessed using the primer-probe set Ag3349, described in Table AVA. Results of the RTQ-PCR runs are shown in Tables AVB, AVC and AVD.

Table AVA. Probe Name Ag3349

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5'-acaaaaatgatggcgatatttag-3' | 22 | 237 | 538 |
| Probe | TET-5'-cgcttccattcaacttcaacaccct-3' - TAMRA | 25 | 270 | 539 |
| Reverse | 5'-tcattcttatccactccagaa-3' | 22 | 295 | 540 |

Table AVB. CNS_neurodegeneration_v1.0

| Tissue Name | Rel. Exp.(%) Ag3349, Run 210141483 | Tissue Name | Rel. Exp.(%) Ag3349, Run 210141483 |
|-------------|---------------------------------------|----------------------------------|---------------------------------------|
| AD 1 Hippo | 32.8 | Control (Path) 3 Temporal Ctx | 0.0 |
| AD 2 Hippo | 61.6 | Control (Path) 4 Temporal Ctx | 48.6 |
| AD 3 Hippo | 18.0 | AD 1 Occipital Ctx | 10.5 |

| | | | |
|------------|------|--------------------|-----|
| AD 5 Hippo | 11.7 | AD 3 Occipital Ctx | 0.0 |
| AD 6 Hippo | | AD 4 Occipital Ctx | |

| | | | |
|-------------------------------|------|--------------------------------|-------|
| Control 2 Hippo | 27.4 | AD 5 Occipital Ctx | 8.6 |
| Control 4 Hippo | 17.9 | AD 6 Occipital Ctx | 0.0 |
| Control (Path) 3 Hippo | 12.7 | Control 1 Occipital Ctx | 0.0 |
| AD 1 Temporal Ctx | 14.8 | Control 2 Occipital Ctx | 0.0 |
| AD 2 Temporal Ctx | 8.7 | Control 3 Occipital Ctx | 51.4 |
| AD 3 Temporal Ctx | 8.2 | Control 4 Occipital Ctx | 5.6 |
| AD 4 Temporal Ctx | 10.4 | Control (Path) 1 Occipital Ctx | 100.0 |
| AD 5 Inf Temporal Ctx | 7.2 | Control (Path) 2 Occipital Ctx | 17.8 |
| AD 5 SupTemporal Ctx | 7.4 | Control (Path) 3 Occipital Ctx | 0.0 |
| AD 6 Inf Temporal Ctx | 9.1 | Control (Path) 4 Occipital Ctx | 41.2 |
| AD 6 Sup Temporal Ctx | 27.9 | Control 1 Parietal Ctx | 3.3 |
| Control 1 Temporal Ctx | 9.2 | Control 2 Parietal Ctx | 70.7 |
| Control 2 Temporal Ctx | 25.9 | Control 3 Parietal Ctx | 14.3 |
| Control 3 Temporal Ctx | 13.4 | Control (Path) 1 Parietal Ctx | 35.8 |
| Control 4 Temporal Ctx | 3.7 | Control (Path) 2 Parietal Ctx | 17.7 |
| Control (Path) 1 Temporal Ctx | 53.2 | Control (Path) 3 Parietal Ctx | 0.0 |
| Control (Path) 2 Temporal Ctx | 51.1 | Control (Path) 4 Parietal Ctx | 52.1 |

Table AVC. General_screening_panel_v1.4

| Tissue Name | Rel. Exp.(%) Ag3349, Run 215620671 | Tissue Name | Rel. Exp.(%) Ag3349, Run 215620671 |
|-------------------------|---------------------------------------|-------------------------|---------------------------------------|
| Adipose | 3.6 | Renal ca. TK-10 | 1.9 |
| Melanoma* Hs688(A).T | 4.5 | Bladder | 35.4 |
| Melanoma* | | Gastric ca (liver met.) | |
| Melanoma* LOXIMVI | 0.5 | Colon ca SW-948 | 2.8 |

| | | | |
|-------------------------------|-------|----------------------------------|------|
| Melanoma* SK-MEL-5 | 8.0 | Colon ca. SW480 | 10.2 |
| Squamous cell carcinoma SCC-4 | 0.0 | Colon ca.* (SW480 met) SW620 | 13.5 |
| Testis Pool | 5.4 | Colon ca. HT29 | 0.0 |
| Prostate ca.* (bone met) PC-3 | 0.8 | Colon ca. HCT-116 | 0.7 |
| Prostate Pool | 15.1 | Colon ca. CaCo-2 | 3.0 |
| Placenta | 0.0 | Colon cancer tissue | 7.0 |
| Uterus Pool | 0.4 | Colon ca. SW1116 | 0.2 |
| Ovarian ca. OVCAR-3 | 0.9 | Colon ca. Colo-205 | 0.8 |
| Ovarian ca. SK-OV-3 | 18.4 | Colon ca. SW-48 | 0.0 |
| Ovarian ca. OVCAR-4 | 0.0 | Colon Pool | 5.3 |
| Ovarian ca. OVCAR-5 | 10.4 | Small Intestine Pool | 2.7 |
| Ovarian ca. IGROV-1 | 0.3 | Stomach Pool | 5.8 |
| Ovarian ca. OVCAR-8 | 1.3 | Bone Marrow Pool | 1.7 |
| Ovary | 5.0 | Fetal Heart | 2.0 |
| Breast ca. MCF-7 | 1.0 | Heart Pool | 2.4 |
| Breast ca. MDA-MB-231 | 1.3 | Lymph Node Pool | 8.9 |
| Breast ca. BT 549 | 0.4 | Fetal Skeletal Muscle | 2.7 |
| Breast ca. T47D | 9.0 | Skeletal Muscle Pool | 0.0 |
| Breast ca. MDA-N | 1.6 | Spleen Pool | 0.4 |
| Breast Pool | 10.5 | Thymus Pool | 10.5 |
| Trachea | 1.2 | CNS cancer (glio/astro) U87-MG | 11.4 |
| Lung | 1.3 | CNS cancer (glio/astro) U-118-MG | 2.4 |
| Fetal Lung | 7.6 | CNS cancer (neuro;met) SK-N-AS | 0.1 |
| Lung ca. NCI-N417 | 0.3 | CNS cancer (astro) SF-539 | 0.2 |
| Lung ca. LX-1 | 100.0 | CNS cancer (astro) SNB-75 | 4.6 |

| Lung ca. SFP-7 | NS cancer tissue |
|----------------|------------------|
| Lung ca. A549 | 0.8 |

| | | | |
|-------------------|------|-------------------------------|-----|
| Lung ca. NCI-H526 | 0.0 | Brain (cerebellum) | 0.9 |
| Lung ca. NCI-H23 | 7.1 | Brain (fetal) | 1.6 |
| Lung ca. NCI-H460 | 0.8 | Brain (Hippocampus) Pool | 0.8 |
| Lung ca. HOP-62 | 2.6 | Cerebral Cortex Pool | 2.3 |
| Lung ca. NCI-H522 | 0.4 | Brain (Substantia nigra) Pool | 2.2 |
| Liver | 0.0 | Brain (Thalamus) Pool | 2.8 |
| Fetal Liver | 10.5 | Brain (whole) | 3.1 |
| Liver ca. HepG2 | 0.8 | Spinal Cord Pool | 4.1 |
| Kidney Pool | 7.9 | Adrenal Gland | 2.4 |
| Fetal Kidney | 47.3 | Pituitary gland Pool | 1.4 |
| Renal ca. 786-0 | 2.6 | Salivary Gland | 1.4 |
| Renal ca. A498 | 0.9 | Thyroid (female) | 0.9 |
| Renal ca. ACHN | 1.3 | Pancreatic ca. CAPAN2 | 3.7 |
| Renal ca. UO-31 | 2.8 | Pancreas Pool | 9.3 |

Table AVD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3349, Run 165222879 | Tissue Name | Rel. Exp.(%) Ag3349, Run 165222879 |
|--------------------------|--|--|--|
| Secondary Th1 act | 0.0 | HUVEC IL-1beta | 0.0 |
| Secondary Th2 act | 0.0 | HUVEC IFN gamma | 0.0 |
| Secondary Tr1 act | 0.8 | HUVEC TNF alpha + IFN gamma | 0.0 |
| Secondary Th1 rest | 0.0 | HUVEC TNF alpha + IL4 | 0.0 |
| Secondary Th2 rest | 0.0 | HUVEC IL-11 | 0.0 |
| Secondary Tr1 rest | 0.0 | Lung Microvascular EC none | 2.3 |
| Primary Th1 act | 0.0 | Lung Microvascular EC TNFalpha + IL-1beta | 0.0 |
| Primary Th2 act | 0.0 | Microvascular Dermal EC none | 2.3 |
| Primary Tr1 act | 0.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 0.6 |
| Primary Th1 rest | 0.0 | Bronchial epithelium TNFalpha + IL1beta | 0.0 |
| Primary Th2 rest | 0.7 | Small airway epithelium none | 0.4 |
| D45RA CD4 lymphocyte act | 0.0 | Coronery artery SMC rest | 0.6 |

| | | | |
|--------------------------------|-----|---|-----|
| CD45RO CD4 lymphocyte act | 0.0 | Coronery artery SMC TNFalpha + IL-1beta | 0.0 |
| CD8 lymphocyte act | 0.0 | Astrocytes rest | 0.0 |
| Secondary CD8 lymphocyte rest | 0.0 | Astrocytes TNFalpha + IL-1beta | 1.0 |
| Secondary CD8 lymphocyte act | 0.0 | KU-812 (Basophil) rest | 0.0 |
| CD4 lymphocyte none | 0.0 | KU-812 (Basophil) PMA/ionomycin | 0.0 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 0.0 | CCD1106 (Keratinocytes) none | 0.6 |
| LAK cells rest | 1.4 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 0.0 |
| LAK cells IL-2 | 0.0 | Liver cirrhosis | 3.3 |
| LAK cells IL-2+IL-12 | 0.0 | Lupus kidney | 5.8 |
| LAK cells IL-2+IFN gamma | 1.0 | NCI-H292 none | 0.6 |
| LAK cells IL-2+ IL-18 | 0.0 | NCI-H292 IL-4 | 0.0 |
| LAK cells PMA/ionomycin | 1.3 | NCI-H292 IL-9 | 1.5 |
| NK Cells IL-2 rest | 0.0 | NCI-H292 IL-13 | 0.8 |
| Two Way MLR 3 day | 0.0 | NCI-H292 IFN gamma | 0.3 |
| Two Way MLR 5 day | 0.0 | HPAEC none | 0.7 |
| Two Way MLR 7 day | 1.0 | HPAEC TNF alpha + IL-1 beta | 0.0 |
| PBMC rest | 0.0 | Lung fibroblast none | 0.0 |
| PBMC PWM | 0.0 | Lung fibroblast TNF alpha + IL-1 beta | 0.6 |
| PBMC PHA-L | 0.0 | Lung fibroblast IL-4 | 0.0 |
| Ramos (B cell) none | 0.0 | Lung fibroblast IL-9 | 0.9 |
| Ramos (B cell) ionomycin | 0.6 | Lung fibroblast IL-13 | 0.0 |
| B lymphocytes PWM | 0.0 | Lung fibroblast IFN gamma | 0.0 |
| B lymphocytes CD40L and IL-4 | 0.0 | Dermal fibroblast CCD1070 rest | 0.6 |
| EOL-1 dbcAMP | 0.0 | Dermal fibroblast CCD1070 TNF alpha | 0.8 |
| EOL-1 dbcAMP PMA/ionomycin | 0.0 | Dermal fibroblast CCD1070 IL-1 beta | 0.0 |

| | | | | |
|---------------------------|-----|---------------------------|---------------|-----|
| Dendritic cells anti-CD40 | 2.9 | Rectal Tissue Macrophages | IBD Colitis 2 | 0.0 |
|---------------------------|-----|---------------------------|---------------|-----|

| | | | |
|-----------------------|-----|--------------------|-------|
| Monocytes rest | 0.0 | IBD Crohn's | 0.0 |
| Monocytes LPS | 1.3 | Colon | 0.6 |
| Macrophages rest | 0.9 | Lung | 0.7 |
| Macrophages LPS | 0.2 | Thymus | 100.0 |
| HUVEC none | 0.0 | Kidney | 1.7 |
| HUVEC starved | 0.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3349 This panel confirms the expression of CG57851-01 gene at low levels in the brains of an independent group of individuals.

However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. The expression of this gene in the brain suggests that therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

General_screening_panel_v1.4 Summary: Ag3349 Highest expression of the CG57851-01 gene is seen in a lung cancer cell line (CT=30). Thus, expression of this gene may be used to differentiate between this sample and other samples on this panel and as a marker for lung cancer. This gene encodes a sulfotransferase homolog. Sulfotransferases are involved in the metabolism of drugs and endogenous compounds in the body and also synthesize the complex glycoproteins found on the cell surface of cancer cells. Therefore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of lung cancer.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in adipose and pancreas. This expression among these tissues suggests that this gene product may play a role in normal metabolic function and that deregulated expression of this gene may contribute to metabolic diseases, such as obesity and diabetes.

Panel 4D Summary: Ag3349 Highest expression of the CG57851-01 gene is seen in the thymus (CT=29.7). The putative protein encoded by this gene could therefore play an important role in T cell development. Small molecule therapeutics designed against the protein encoded by this gene could be utilized to modulate immune function (T cell development) and be important for organ transplant, AIDS treatment or post chemotherapy immune

Panel 5 Islet Summary: Ag3349 Expression of the CG57851-01 gene was undetectable in all samples on this panel (CTs >35). (Data not shown.)

AW. CG59258-01: KIAA1608 protein

Expression of gene CG59258-01 was assessed using the primer-probe set Ag3520, described in Table AWA.

Table AWA. Probe Name Ag3520

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|---|--------|----------------|------------|
| Forward | 5' - cctcacagatgaggacacaga - 3' | 21 | 717 | 541 |
| Probe | TET - 5' - acttgcttgc当地aaagtcaactcagcaa - 3' - TAMRA | 26 | 752 | 542 |
| Reverse | 5' - tttctgagagccagacagacat - 3' | 22 | 781 | 543 |

CNS_neurodegeneration_v1.0 Summary: Ag3520 Expression of the CG59258-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3520 Expression of the CG59258-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel 4D Summary: Ag3520 Expression of the CG59258-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

AX. CG59564-01: Sorting nexin 6

Expression of gene CG59564-01 was assessed using the primer-probe set Ag3471, described in Table AXA. Results of the RTQ-PCR runs are shown in Tables AXB, AXC and AXD.

Table AXA. Probe Name Ag3471

| Primers | Sequences | Length | Start Position | SEQ ID NO: |
|---------|--|--------|----------------|------------|
| Forward | 5' - gtgcctggcagacgattata - 3' | 20 | 820 | 544 |
| Probe | TET - 5' - ctatctcagctgc当地gtgagcagtctg - 3' - TAMRA | 26 | 843 | 545 |
| Reverse | 5' - gtccttagctggttgacttcct - 3' | 22 | 876 | 546 |

| Tissue Name | Rel. Exp.(%) Ag3471, Run 210376963 | Tissue Name | Rel. Exp.(%) Ag3471, Run 210376963 |
|-------------|---------------------------------------|-------------|---------------------------------------|
|-------------|---------------------------------------|-------------|---------------------------------------|

| | | | |
|----------------------------------|------|-----------------------------------|-------|
| AD 1 Hippo | 10.8 | Control (Path) 3 Temporal Ctx | 2.4 |
| AD 2 Hippo | 27.0 | Control (Path) 4 Temporal Ctx | 28.5 |
| AD 3 Hippo | 5.9 | AD 1 Occipital Ctx | 10.3 |
| AD 4 Hippo | 10.8 | AD 2 Occipital Ctx (Missing) | 0.0 |
| AD 5 Hippo | 64.6 | AD 3 Occipital Ctx | 3.6 |
| AD 6 Hippo | 43.8 | AD 4 Occipital Ctx | 30.4 |
| Control 2 Hippo | 56.3 | AD 5 Occipital Ctx | 100.0 |
| Control 4 Hippo | 4.0 | AD 6 Occipital Ctx | 14.5 |
| Control (Path) 3 Hippo | 2.3 | Control 1 Occipital Ctx | 1.1 |
| AD 1 Temporal Ctx | 11.5 | Control 2 Occipital Ctx | 82.9 |
| AD 2 Temporal Ctx | 36.3 | Control 3 Occipital Ctx | 13.3 |
| AD 3 Temporal Ctx | 4.7 | Control 4 Occipital Ctx | 5.4 |
| AD 4 Temporal Ctx | 27.9 | Control (Path) 1 Occipital Ctx | 87.7 |
| AD 5 Inf Temporal Ctx | 85.9 | Control (Path) 2 Occipital Ctx | 10.3 |
| AD 5 Sup Temporal Ctx | 37.1 | Control (Path) 3 Occipital Ctx | 1.5 |
| AD 6 Inf Temporal Ctx | 46.3 | Control (Path) 4 Occipital Ctx | 12.2 |
| AD 6 Sup Temporal Ctx | 52.1 | Control 1 Parietal Ctx | 3.1 |
| Control 1 Temporal Ctx | 3.6 | Control 2 Parietal Ctx | 38.4 |
| Control 2 Temporal Ctx | 81.2 | Control 3 Parietal Ctx | 17.4 |
| Control 3 Temporal Ctx | 19.1 | Control (Path) 1 Parietal Ctx | 88.9 |
| Control 3 Temporal Ctx | 8.0 | Control (Path) 2 Parietal Ctx | 22.2 |
| Control (Path) 1 Temporal Ctx | 88.9 | Control (Path) 3 Parietal Ctx | 1.7 |
| Control (Path) 2 Temporal Ctx | 48.0 | Control (Path) 4 Parietal Ctx | 38.7 |

| Tissue Name | Rel. Exp.(%) Ag3471, | Tissue Name | Rel. Exp.(%) Ag3471, |
|-------------|----------------------|-------------|----------------------|
|-------------|----------------------|-------------|----------------------|

| | Run 222691297 | | Run 222691297 |
|-------------------------------|----------------------|-------------------------------------|----------------------|
| Adipose | 2.3 | Renal ca. TK-10 | 2.7 |
| Melanoma* Hs688(A).T | 3.1 | Bladder | 4.2 |
| Melanoma* Hs688(B).T | 4.2 | Gastric ca. (liver met.) NCI-N87 | 6.3 |
| Melanoma* M14 | 13.0 | Gastric ca. KATO III | 4.1 |
| Melanoma* LOXIMVI | 0.7 | Colon ca. SW-948 | 0.7 |
| Melanoma* SK-MEL-5 | 0.8 | Colon ca. SW480 | 2.6 |
| Squamous cell carcinoma SCC-4 | 1.5 | Colon ca.* (SW480 met) SW620 | 4.5 |
| Testis Pool | 6.2 | Colon ca. HT29 | 2.2 |
| Prostate ca.* (bone met) PC-3 | 3.8 | Colon ca. HCT-116 | 3.9 |
| Prostate Pool | 0.7 | Colon ca. CaCo-2 | 3.5 |
| Placenta | 2.3 | Colon cancer tissue | 1.0 |
| Uterus Pool | 0.7 | Colon ca. SW1116 | 1.9 |
| Ovarian ca. OVCAR-3 | 5.3 | Colon ca. Colo-205 | 0.6 |
| Ovarian ca. SK-OV-3 | 2.1 | Colon ca. SW-48 | 2.3 |
| Ovarian ca. OVCAR-4 | 2.8 | Colon Pool | 7.0 |
| Ovarian ca. OVCAR-5 | 5.8 | Small Intestine Pool | 5.8 |
| Ovarian ca. IGROV-1 | 5.3 | Stomach Pool | 5.5 |
| Ovarian ca. OVCAR-8 | 3.0 | Bone Marrow Pool | 3.5 |
| Ovary | 7.1 | Fetal Heart | 1.7 |
| Breast ca. MCF-7 | 2.2 | Heart Pool | 3.1 |
| Breast ca. MDA-MB-231 | 2.4 | Lymph Node Pool | 9.5 |
| Breast ca. BT 549 | 98.6 | Fetal Skeletal Muscle | 1.4 |
| Breast ca. T47D | 8.4 | Skeletal Muscle Pool | 4.2 |
| Breast ca. MDA-N | 4.5 | Spleen Pool | 1.8 |
| Breast Pool | 7.5 | Thymus Pool | 6.2 |
| Fetal brain | ~ ~ | CNS cancer (glio/astro) | ~ ~ |

| | | 13.4 | 11.5 |
|------------|--|------------|------|
| Fetal Lung | | CNS cancer | |

| | | (neuro;met) SK-N-AS | |
|-------------------|------|-------------------------------|--------------|
| Lung ca. NCI-N417 | 2.2 | CNS cancer (astro) SF-539 | 1.9 |
| Lung ca. LX-1 | 2.2 | CNS cancer (astro) SNB-75 | 23.8 |
| Lung ca. NCI-H146 | 2.1 | CNS cancer (glio) SNB-19 | 3.6 |
| Lung ca. SHP-77 | 3.7 | CNS cancer (glio) SF-295 | 11.3 |
| Lung ca. A549 | 3.7 | Brain (Amygdala) Pool | 22.1 |
| Lung ca. NCI-H526 | 2.5 | Brain (cerebellum) | 42.9 |
| Lung ca. NCI-H23 | 17.6 | Brain (fetal) | 100.0 |
| Lung ca. NCI-H460 | 1.8 | Brain (Hippocampus) Pool | 26.6 |
| Lung ca. HOP-62 | 3.6 | Cerebral Cortex Pool | 33.0 |
| Lung ca. NCI-H522 | 5.7 | Brain (Substantia nigra) Pool | 29.3 |
| Liver | 0.1 | Brain (Thalamus) Pool | 37.4 |
| Fetal Liver | 1.3 | Brain (whole) | 55.1 |
| Liver ca. HepG2 | 1.3 | Spinal Cord Pool | 7.7 |
| Kidney Pool | 10.6 | Adrenal Gland | 1.5 |
| Fetal Kidney | 6.7 | Pituitary gland Pool | 0.6 |
| Renal ca. 786-0 | 0.9 | Salivary Gland | 0.8 |
| Renal ca. A498 | 0.8 | Thyroid (female) | 0.8 |
| Renal ca. ACHN | 2.1 | Pancreatic ca. CAPAN2 | 3.0 |
| Renal ca. UO-31 | 3.4 | Pancreas Pool | 7.4 |

Table AXD. Panel 4D

| Tissue Name | Rel. Exp.(%) Ag3471, Run 166417126 | Tissue Name | Rel. Exp.(%) Ag3471, Run 166417126 |
|--------------------|--|-----------------------------|--|
| Secondary Th1 act | 10.2 | HUVEC IL-1beta | 2.3 |
| Secondary Th2 act | 11.2 | HUVEC IFN gamma | 7.8 |
| Secondary Tr1 act | 19.2 | HUVEC TNF alpha + IFN gamma | 4.7 |
| Secondary Th1 rest | 28.7 | HUVEC TNF alpha + IL4 | 6.3 |
| Secondary Th2 rest | 18.4 | HUVEC IL-11 | 6.2 |
| Secondary Tr1 rest | 24.5 | Lung Microvascular EC | 6.4 |

| | | | |
|-----------------|------|---------------------------------|-----|
| Primary Th2 act | 20.4 | Microvascular Dermal EC none | 6.9 |
|-----------------|------|---------------------------------|-----|

| | | | |
|--------------------------------|------|--|------|
| Primary Tr1 act | 31.0 | Microvasular Dermal EC TNFalpha + IL-1beta | 2.5 |
| Primary Th1 rest | 45.7 | Bronchial epithelium TNFalpha + IL1beta | 2.6 |
| Primary Th2 rest | 23.3 | Small airway epithelium none | 3.1 |
| Primary Tr1 rest | 25.3 | Small airway epithelium TNFalpha + IL-1beta | 3.3 |
| CD45RA CD4 lymphocyte act | 9.7 | Coronery artery SMC rest | 3.9 |
| CD45RO CD4 lymphocyte act | 23.2 | Coronery artery SMC TNFalpha + IL-1beta | 4.6 |
| CD8 lymphocyte act | 9.0 | Astrocytes rest | 12.7 |
| Secondary CD8 lymphocyte rest | 24.8 | Astrocytes TNFalpha + IL-1beta | 18.9 |
| Secondary CD8 lymphocyte act | 19.9 | KU-812 (Basophil) rest | 26.2 |
| CD4 lymphocyte none | 10.6 | KU-812 (Basophil) PMA/ionomycin | 50.0 |
| 2ry Th1/Th2/Tr1_anti-CD95 CH11 | 22.7 | CCD1106 (Keratinocytes) none | 6.9 |
| LAK cells rest | 6.4 | CCD1106 (Keratinocytes) TNFalpha + IL-1beta | 10.9 |
| LAK cells IL-2 | 27.5 | Liver cirrhosis | 15.3 |
| LAK cells IL-2+IL-12 | 21.3 | Lupus kidney | 4.2 |
| LAK cells IL-2+IFN gamma | 27.4 | NCI-H292 none | 5.8 |
| LAK cells IL-2+ IL-18 | 22.7 | NCI-H292 IL-4 | 7.2 |
| LAK cells PMA/ionomycin | 8.2 | NCI-H292 IL-9 | 3.6 |
| NK Cells IL-2 rest | 13.6 | NCI-H292 IL-13 | 3.7 |
| Two Way MLR 3 day | 23.7 | NCI-H292 IFN gamma | 3.2 |
| Two Way MLR 5 day | 5.6 | HPAEC none | 3.7 |
| Two Way MLR 7 day | 7.7 | HPAEC TNF alpha + IL-1 beta | 2.3 |
| PBMC rest | 6.1 | Lung fibroblast none | 18.3 |
| PBMC PWM | 7.3 | Lung fibroblast TNF alpha + IL-1 beta | 20.6 |
| PBMC PHA-L | 7.1 | Lung fibroblast IL-4 | 16.6 |
| Ramos (B cell) none | 6.3 | Lung fibroblast IL-9 | 9.2 |

Ramos (B cell)

B lymphocytes PWM

gamma

| | | | |
|---------------------|------|-------------------|------|
| B lymphocytes CD40L | 11.1 | Dermal fibroblast | 11.4 |
|---------------------|------|-------------------|------|

| | | | |
|-------------------------------|------|--|--------------|
| and IL-4 | | CCD1070 rest | |
| EOL-1 dbcAMP | 7.4 | Dermal fibroblast CCD1070 TNF alpha | 28.5 |
| EOL-1 dbcAMP PMA/ionomycin | 12.5 | Dermal fibroblast CCD1070 IL-1 beta | 7.2 |
| Dendritic cells none | 13.4 | Dermal fibroblast IFN gamma | 6.9 |
| Dendritic cells LPS | 14.0 | Dermal fibroblast IL-4 | 12.8 |
| Dendritic cells anti- CD40 | 15.9 | IBD Colitis 2 | 1.7 |
| Monocytes rest | 21.3 | IBD Crohn's | 4.8 |
| Monocytes LPS | 11.4 | Colon | 100.0 |
| Macrophages rest | 23.5 | Lung | 12.6 |
| Macrophages LPS | 3.7 | Thymus | 8.9 |
| HUVEC none | 6.7 | Kidney | 34.4 |
| HUVEC starved | 11.0 | | |

CNS_neurodegeneration_v1.0 Summary: Ag3471 This panel does not show differential expression of the CG59564-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.4 for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3471 The CG59564-01 gene, a sorting nexin homolog, shows highly brain preferential expression. Moderate levels of expression are seen in all brain regions examined, with highest expression in the fetal brain (CT=28.5). Thus, this gene would be useful for distinguishing brain tissue from non-neural tissue, and may be beneficial as a drug target in neurologic disease, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Among tissues with metabolic function, this gene is expressed at low levels in pituitary, adipose, adrenal gland, pancreas, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that deregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

In addition, this gene is expressed at significant levels in a breast cancer cell line

samples of this panel are available through the MGI